

A

SEQUENCE LISTING



#5

<110> Edinger, Shlomit R
Gerlach, Valerie
MacDougall, John R
Malyankar, Muriel M
Smithson, Glennnda
Millet, Isabelle
Peyman, John A
Stone, David J
Gunther, Erik
Ellerman, Karen
Shimkets, Richard A
Padigaru, Muralidhara
Guo, Xiaojia
Patilurajan, Meera
Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
Kekuda, Ramesh
Spytek, Kimberly A
Gangolli, Esha A
Fernandes, Elma R
Gorman, Linda

<120> Proteins and Nucleic Acids Encoding Same

<130> 21402-168

<140> 09/981,151

<141> 2001-10-16

<150> 60/241,040

<151> 2000-10-17

<150> 60/241,058

<151> 2000-10-17

<150> 60/241,063

<151> 2000-10-17

<150> 60/241,243

<151> 2000-10-17

<150> 60/242,152

<151> 2000 10-20

<150> 60/242,482

<151> 2000-10-23

<150> 60/242,611

<151> 2000-10-23

<150> 60/242,612

<151> 2000-10-23

<150> 60/242,880

<151> 2000-10-24

<150> 60/242,881

<151> 2000-10-24

<150> 60/259,028

<151> 2000-12-29

<150> 60/269,813

<151> 2001-02-20

<150> 60/286,324

<151> 2001-04-25

<150> 60/294,108

<151> 2001-05-29

<150> 60/303,968

<151> 2001-07-09

<160> 160

<170> PatentIn Ver. 2.1

<210> 1

<211> 2997

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (857)..(858)

<223> Wherein n is an a or t or c or g.

<400> 1

```
cgctcctgga tgaagccccg cgcgcgcgga tggcggggct tggcggcgct gtggatgctg 60
ttggcgcagg tggcgcagca ggtgagtcctc gggcgctccc accagcgcgg aaaccgcggg 120
tccggacagc tggaggcgag tccccgcgg ctcctctccc gcggaccccg ccgtctcacc 180
gcgatgtcgc cgctgttttc cgcaggcacc tgcgtgcgcc atgggacccg cagcggcagc 240
gcctgggagc ccgagcgtcc cgcgtcctcc tccaccgcg gagcggcccg gctggatgga 300
aaagggcggg acatggatga agctggaac catcgttctc agcaaaactaa cacaggaaca 360
gaaaaccaa cactgcatgt tctcactcaa tatgacctg tctctgccta cgaggttgac 420
cacaggggcg attacgtgtc ccatgaaatc atgcaccatc agcggcggag aagagcagtg 480
gccgtgtccg aggttgagtc tcttcacctt cggttgaaa gcccaggca cgacttcac 540
atggatctga ggacttcacg cagcctagt gctcctggct ttattgtgca gacgttgga 600
aagacaggca ctaagtctgt gcagacttta ccgcccaggg acttctgttt ctatcaaggc 660
tctttgcgat cacacagaaa ctcgccatcg catggaggga agttctgtga gggctccact 720
cgcactctga agctctgcaa cagtcagaaa tgtcccggg acagtgttga ctccgtgct 780
gctcagtgtg ccgagcacia cagcagacga ttcagagggc ggcactacaa gtggaagcct 840
tacctcaag tagaagnnga cttatgcaaa ctctactgta tcgcagaagg atttgatttc 900
ttcttttctt tgtcaataaa agtcaaagat gggactccat gctcggagga tagccgtaat 960
gtttgtatag atgggatatg tgagctcagt gtggtgtcca catctgcgca catgccccag 1020
cctccaagg aagacctctt catcttgcca gatgagtata agtcttgctt acggcataag 1080
cgctctcttc tgagggtccc tagaaatgaa gaactgaacg tggagacctt ggtggtggtc 1140
gacaaaaaga tgatgcaaaa ccatggccat gaaaatatca ccacctacgt gctcacgata 1200
ctcaacatgg tatctgcttt attcaaagat ggaacaatag gaggaaacat caacattgca 1260
attgtaggtc tgattcttct agaagatgaa cagccaggac tgggtgataag tcaccacgca 1320
```

gaccacacct taagtagctt ctgccagtgg cagtctggat tgatggggaa agatgggact 1380
cgatcatgacc acgccatctt actgactggg ctggatatat gttcctggaa gaatgagccc 1440
tgtgacactt tgggatttgc acccataagt ggaatgtgta gtaaataatcg cagctgcacg 1500
attaatgaag atacaggtct tggactggcc ttcaccattg cccatgagtc tggacacaac 1560
tttggcatga ttcattgatg agaagggaac atgtgtaaaa agtccgaggg caacatcatg 1620
tcccctacat tggcaggacg caatggagtc ttctcctggg caccctgcag ccgccagtat 1680
ctacacaaat ttctaagcac cgtcaagct atctgccttg ctgacagcc aaagcctgtg 1740
aaggaatata agtatcctga gaaattgccg ggagaattat atgatgcaa cacacagtgc 1800
aagtggcagt tcggagagaa agccaagctc tgcattgctg actttaaaaa ggacatctgt 1860
aaagccctgt ggtgccatcg tattggaagg aaatgtgaga cttaaatttat gccagcagca 1920
gaaggcacia tttgtgggca tgacatgtgg tgccggggag gacagtgtgt gaaatatggt 1980
gatgaaggcc ccaagcccac ccatggccac tggctggact ggtcttcttg gtccccatgc 2040
tccaggacct gcggaggggg agtatctcat aggagtcgcc tctgcaccaa ccccaatcca 2100
tcgcatggag ggaagtcttg tgagggctcc actcgcactc tgaagctctg caacagtcag 2160
aaatgtcccc gggacagtgt tgacttccgt gctgctcagt gtgccgagca caacagcaga 2220
cgattcagag ggcggcacta caagtggaa cctcaggact tatgcaaact ctactgtatc 2280
gcagaaggat ttgatttctt cttttctttg tcaaataaag tcaaagatgg gactccatgc 2340
tcggaggata gccgtaattg ttgtatagat gggatatgtg agnttggatg tgacaatgtc 2400
cttgatctg atgctgttga agacgtctgt ggggtgtgta acgggaataa ctcagcctgc 2460
acgattcaca ggggtctcta caccaagcac caccacacca accattatca catggtcacc 2520
attccttctg gagcccgag tatccgcac tatgaaatga acgtctctac ctctacatt 2580
tctgtgcgca atgccctcag aaggactact ctgaatgggc actggaccgt ggactggccc 2640
ggccggtaca aatttccggg cactactttc gactacagac ggtcctataa tgagcccgag 2700
aacttaatcg ctactggacc aaccaacgag aactgattg tggagctgct gtttcaggga 2760
aggaaccggt gtgttgctg ggaatactcc atgcctcgtc tggggaccga gaagcagccc 2820
cctgccagc ccagctacac ttgggccatc gtgcgctctg agtgctccgt gtctgcgga 2880
gggggtaggt gccttccagt gctgctcctg gaggcagcat gtcagccttc agccactgag 2940
tacattgcac tggcctttct tgaatcctaa tgagcagccc ggngetttct cctgcca 2997

<210> 2

<211> 986

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (283)

<223> Wherein Xaa is any amino acid.

<400> 2

Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
1 5 10 15

Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
20 25 30

Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
35 40 45

Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
50 55 60

Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
65 70 75 80

Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp

				85				90				95			
Gly	Lys	Gly	Arg	Asp	Met	Asp	Glu	Ala	Gly	Asn	His	Arg	Ser	Gln	Gln
			100				105						110		
Thr	Asn	Thr	Gly	Thr	Glu	Asn	Gln	Thr	Leu	His	Val	Leu	Thr	Gln	Tyr
			115				120				125				
Asp	Leu	Val	Ser	Ala	Tyr	Glu	Val	Asp	His	Arg	Gly	Asp	Tyr	Val	Ser
			130				135				140				
His	Glu	Ile	Met	His	His	Gln	Arg	Arg	Arg	Arg	Ala	Val	Ala	Val	Ser
			150						155			160			
Glu	Val	Glu	Ser	Leu	His	Leu	Arg	Leu	Lys	Gly	Pro	Arg	His	Asp	Phe
			165						170			175			
His	Met	Asp	Leu	Arg	Thr	Ser	Ser	Ser	Leu	Val	Ala	Pro	Gly	Phe	Ile
			180						185			190			
Val	Gln	Thr	Leu	Gly	Lys	Thr	Gly	Thr	Lys	Ser	Val	Gln	Thr	Leu	Pro
			195						200			205			
Pro	Glu	Asp	Phe	Cys	Phe	Tyr	Gln	Gly	Ser	Leu	Arg	Ser	His	Arg	Asn
			210			215			220						
Ser	Pro	Ser	His	Gly	Gly	Lys	Phe	Cys	Glu	Gly	Ser	Thr	Arg	Thr	Leu
			225			230			235			240			
Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro	Arg	Asp	Ser	Val	Asp	Phe	Arg
			245						250			255			
Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	Phe	Arg	Gly	Arg	His
			260						265			270			
Tyr	Lys	Trp	Lys	Pro	Tyr	Thr	Gln	Val	Glu	Xaa	Asp	Leu	Cys	Lys	Leu
			275			280			285						
Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	Lys
			290			295			300						
Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	Ile
			305			310			315			320			
Asp	Gly	Ile	Cys	Glu	Leu	Ser	Val	Val	Ser	Thr	Ser	Ala	His	Met	Pro
			325						330			335			
Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys	Ser
			340			345			350						
Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu	Glu
			355			360			365						
Leu	Asn	Val	Glu	Thr	Leu	Val	Val	Val	Asp	Lys	Lys	Met	Met	Gln	Asn
			370			375			380						
His	Gly	His	Glu	Asn	Ile	Thr	Thr	Tyr	Val	Leu	Thr	Ile	Leu	Asn	Met

385		390		395		400
Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn Ile						
	405			410		415
Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu Val						
	420			425		430
Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp Gln						
	435			440		445
Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile Leu						
	450			455		460
Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp Thr						
	465			470		475
Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser Cys						
	485			490		495
Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala His						
	500			505		510
Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn Met						
	515			520		525
Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly Arg						
	530			535		540
Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His Lys						
	545			550		555
Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys Pro						
	565			570		575
Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr Asp						
	580			585		590
Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu Cys						
	595			600		605
Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His Arg						
	610			615		620
Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly Thr						
	625			630		635
Ile Cys Gly His Asp Met Trp Cys Arg Gly Gly Gln Cys Val Lys Tyr						
	645			650		655
Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser						
	660			665		670
Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His Arg						
	675			680		685
Ser Arg Leu Cys Thr Asn Pro Asn Pro Ser His Gly Gly Lys Phe Cys						

690	695	700
Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro		
705	710	715 720
Arg Asp Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn Ser		
	725	730 735
Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Gln Asp Leu Cys		
	740	745 750
Lys Leu Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser		
	755	760 765
Asn Lys Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val		
	770	775 780
Cys Ile Asp Gly Ile Cys Glu Xaa Gly Cys Asp Asn Val Leu Gly Ser		
	785	790 795 800
Asp Ala Val Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala		
	805	810 815
Cys Thr Ile His Arg Gly Leu Tyr Thr Lys His His His Thr Asn His		
	820	825 830
Tyr His Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr		
	835	840 845
Glu Met Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg		
	850	855 860
Arg Tyr Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr		
	865	870 875 880
Lys Phe Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro		
	885	890 895
Glu Asn Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu		
	900	905 910
Leu Leu Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met		
	915	920 925
Pro Arg Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr		
	930	935 940
Trp Ala Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg		
	945	950 955 960
Cys Leu Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr		
	965	970 975
Ala Tyr Ile Ala Leu Ala Phe Leu Glu Ser		
	980	985

<210> 3
 <211> 2433
 <212> DNA
 <213> Homo sapiens

<400> 3
 gtggcccccta gcccctcgga gcgctcctgg atgaagcccc gcgcgcgcgg atggcggggc 60
 ttggcggcgc tgtggatgct gctggcgagc gtggccgagc aggtgagtc cgggcgctcc 120
 caccagcgcg gaaaccgcgg gtccggacag ctggaggcga gtccccgcg gctcctctcc 180
 cgcggacccc gccgtctcac cgcgatgtcg ccgctgtttt ccgcaggcac ctgcgtgcgc 240
 catgggaccc gcagcggcag cgcctgggag cccgagcgtc ccgcgtcctc ctccaccgc 300
 ggagcggccg ggctggatgg aaaagggcgg gacatggatg aagctggaaa ccatcgttct 360
 cagcaacta acacaggaac agaaaaccaa aactgcatg ttctcactcg tgaatatgac 420
 ctggtctctg cctacgaggt tgaccacagg ggcgattacg tgtcccatga aatcatgcac 480
 catcagcggc ggagaagagc agtggccgtg tccgaggttg agtctcttca ccttcggctg 540
 aaaggcccca ggcacgactt ccacatggat ctgaggactt ccagcagcct agtggctcct 600
 ggcttttattg tgcagacgtt gggaaaagaca ggcactaagt ctgtgcagac ttaccgcca 660
 gaggacttct gtttctatca aggtctcttg cgtcacaca gaaactcccc atcgcatgga 720
 gggaagttct gtgagggctc cactcgcact ctgaagctct gcaacagtca gaaatgtccc 780
 cgggacagtg ttgacttccg tgctgctcag tgtgccgagc acaacagcag acgattcaga 840
 gggcggcact acaagtggaa gccttacact caagtagaac aggacttatg caaactctac 900
 tgtatcgcag aaggatttga tttcttcttt tctttgtcaa ataaagtcaa agatgggact 960
 ccatgctcgg aggatagccg taatgtttgt atagatggga tatgtgagat gccccagcct 1020
 cccaaggaag acctcttcat cttgccagat gagtataagt cttgcttacg gcataagcgc 1080
 tctcttctga ggtcccatag aaatgaagaa ctgaacgtgg agaccttggg ggtggtcgac 1140
 aaaaagatga tgcaaaacca tggccatgaa aatatcacca cctacgtgct caccgatactc 1200
 aacatggtat ctgctttatt caaagatgga acaataggag gaaacatcaa cattgcaatt 1260
 gtaggtctga ttcttctaga agatgaacag gacatctgta aagccctgtg gtgccatcgt 1320
 attggaagga aatgtgagac taaatttatg ccagcagcag aaggcacaat ttgtgggcat 1380
 gacatgtggt gccggggagg acagtgtgtg aaatatgggt atgaaggccc caagcccacc 1440
 catggccact ggtcggactg gtcttcttgg tccccatgct ccaggacctg cggaggggga 1500
 gtatctcata ggagtcgcct ctgcaccaac cccaggccat cgcattggagg gaagtctgt 1560
 gagggctcca ctgcactct gaagctctgc aacagtcaga aatgtccccg ggacagtgtt 1620
 gacttccgtg ctgctcagtg tgccgagcac aacagcagac gattcagagg gcggcactac 1680
 aagtgaagc ctcaggactt atgcaaaact tactgtatcg cagaaggatt tgatttcttc 1740
 ttttctttgt caaataaagt caaagatggg actccatgct cggaggatag ccgtaatgtt 1800
 tgtatagatg ggatagtga gggatgtgac aatgtccttg gatctgatgc tgttgaagac 1860
 gtctgtgggg tgtgtaacgg gaataactca gcctgcacga ttcacagggg tctctacacc 1920
 aagcaccacc acaccaacta ttatcacatg gtcaccattc cttctggagc ccggagtatc 1980
 cgcacttatg aaatgaacgt ctctacctcc tacatttctg tgcgcaatgc cctcagaagg 2040
 tactacctga atgggactg gaccgtggac tggcccgcc ggtacaaatt ttcgggcact 2100
 actttcgact acagacggtc ctataatgag cccgagaact taatcgctac tggaccaacc 2160
 aacgagacac tgattgtgga gctgctgttt cagggaagga acccggtgtg tgcttgggaa 2220
 tactccatgc ctgcttggg gaccgagaag cagccccctg cccagcccag ctacacttgg 2280
 gccatcgtgc gctctgagtg ctccgtgtcc tgcggagggg gtagggtgct tccagtgtg 2340
 ctcttgaggg cagcatgtca gccttcagcc actgcgtaca ttgcactggc ctttcttgaa 2400
 tcctaattgag cagcccgggg cttctccctg cca 2433

<210> 4
 <211> 791
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
 1 5 10 15

Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
 20 25 30
 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
 35 40 45
 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
 50 55 60
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
 65 70 75 80
 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 85 90 95
 Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
 100 105 110
 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Arg Glu
 115 120 125
 Tyr Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val
 130 135 140
 Ser His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val
 145 150 155 160
 Ser Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp
 165 170 175
 Phe His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe
 180 185 190
 Ile Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu
 195 200 205
 Pro Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg
 210 215 220
 Asn Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr
 225 230 235 240
 Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe
 245 250 255
 Arg Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg
 260 265 270
 His Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Gln Asp Leu Cys Lys
 275 280 285
 Leu Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn
 290 295 300
 Lys Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys
 305 310 315 320

Ile Asp Gly Ile Cys Glu Met Pro Gln Pro Pro Lys Glu Asp Leu Phe
 325 330 335
 Ile Leu Pro Asp Glu Tyr Lys Ser Cys Leu Arg His Lys Arg Ser Leu
 340 345 350
 Leu Arg Ser His Arg Asn Glu Glu Leu Asn Val Glu Thr Leu Val Val
 355 360 365
 Val Asp Lys Lys Met Met Gln Asn His Gly His Glu Asn Ile Thr Thr
 370 375 380
 Tyr Val Leu Thr Ile Leu Asn Met Val Ser Ala Leu Phe Lys Asp Gly
 385 390 395 400
 Thr Ile Gly Gly Asn Ile Asn Ile Ala Ile Val Gly Leu Ile Leu Leu
 405 410 415
 Glu Asp Glu Gln Asp Ile Cys Lys Ala Leu Trp Cys His Arg Ile Gly
 420 425 430
 Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly Thr Ile Cys
 435 440 445
 Gly His Asp Met Trp Cys Arg Gly Gly Gln Cys Val Lys Tyr Gly Asp
 450 455 460
 Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser Ser Trp
 465 470 475 480
 Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His Arg Ser Arg
 485 490 495
 Leu Cys Thr Asn Pro Arg Pro Ser His Gly Gly Lys Phe Cys Glu Gly
 500 505 510
 Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp
 515 520 525
 Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg
 530 535 540
 Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Gln Asp Leu Cys Lys Leu
 545 550 555 560
 Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys
 565 570 575
 Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile
 580 585 590
 Asp Gly Ile Cys Glu Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val
 595 600 605
 Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
 610 615 620

His Arg Gly Leu Tyr Thr Lys His His His Thr Asn Tyr Tyr His Met
 625 630 635 640
 Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met Asn
 645 650 655
 Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr Tyr
 660 665 670
 Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe Ser
 675 680 685
 Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu
 690 695 700
 Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe
 705 710 715 720
 Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu
 725 730 735
 Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile
 740 745 750
 Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu Pro
 755 760 765
 Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr Ile
 770 775 780
 Ala Leu Ala Phe Leu Glu Ser
 785 790

<210> 5
 <211> 2902
 <212> DNA
 <213> Homo sapiens

<400> 5
 ttggcggcgc tgtggatgct gctggcgcag gtggccgagc aggtgagtc cgggcgctcc 60
 caccagcgcg gaaaccgcgg gtccggacag ctggaggcga gtcccccgcg gctcctctcc 120
 cgcggacccc gccgtctcac cgcgatgtcg ccgctgtttt ccgcaggcac ctgcgtgcgc 180
 catgggaccc gcagcggcag cgcctgggag cccgagcgtc ccgcgtcctc ctccagacct 240
 ggtctctgcc tacgaggttg accacagggg cgattacgtg tcccatgaaa tcatgcacca 300
 tcagcggcgg agaagagcag tggccgtgtc cgaggttgag ccagcctttc tccaggtatg 360
 cagagccaga gagctcagac tgtgtgtgga ggcctttccc attgctaatt ctccagccggg 420
 gtttttgaac ctttccaatg ttcgctctca ctggagggaa cagcatgctt ccaagagaat 480
 aataacaaat gcaatgcttg gagaatcggc cctggcttca accagaaagt ctaattgtgt 540
 tttctttctt tctttttatt tttccagtc aggcattgata cgaacagaag aggcagatta 600
 cttcctaagg ccacttcctt cacacctctc atggaaactc ggcagagctg cccaaggcag 660
 ctgcgccatcc cactgtactgt acaagagaga ggtcctggtg acctcaagga catgggagct 720
 ggcacatcaa ccctgcaca gcagcgacct tcgcctggga ctgccacaaa agcagcattt 780
 ctgtggaaga cgcaagaaat acatgccccg gcctcccaag gaagacctct tcatcttgcc 840
 agatgagtat aagtcttgct tacggcataa gcgctctctt ctgaggtccc atagaaatga 900
 agaactgaac gtggagacct tgggtggtgt cgacaaaaag atgatgcaaa accatggcca 960

tgaaaatatac	accacctacg	tgtctcacgat	actcaacatg	gtatctgctt	tattcaaaga	1020
tggaacaata	ggaggaaaca	tcaacattgc	aattgtaggt	ctgattcttc	tagaagatga	1080
acagccagga	ctgggtgataa	gtcaccacgc	agaccacacc	ttaagtagtt	tctgccagtg	1140
gcagtctgga	ttgatgggga	aagatgggac	tcgtcatgac	cacgccatct	tactgactgg	1200
tctggatata	tgttcctgga	agaatgagcc	ctgtgacact	ttgggatttg	cacccataag	1260
tggaatgtgt	agtaaataac	gcagctgcac	gattaatgaa	gatacaggtc	ttggactggc	1320
cttcaccatt	gccccatgag	ctggacacaa	ctttggcatg	attcatgatg	gagaagggaa	1380
catgtgcaaa	aagtcggagg	gcaacatcat	gtcccttaca	ttggcaggac	gcaatggagt	1440
cttctcctgg	tcaccctgca	gccgccagta	tctacacaaa	tttctaagca	ccgctcaagc	1500
tatctgcctt	gctgatcagc	caaagcctgt	gaaggaatac	aagtatcctg	agaaattgcc	1560
aggagaatta	tatgggtgcaa	acacacagtg	caagtggcag	ttcggagaga	aagccaagct	1620
ctgcatgctg	gacttttaaaa	aggacatctg	taaagccctg	tgggtgccatc	gtattggaag	1680
gaaatgtgag	actaaattta	tgccagcagc	agaaggcaca	atthgtgggc	atgaacatgg	1740
tgccggagga	cagtgtgtga	aatatgggtg	tgaaggcccc	aagcccaccc	atggccactg	1800
gtcggactgg	tcttcttggg	ccccatgctc	caggacctgc	ggagggggag	tatctcatag	1860
gagtcgctct	caaaaatacac	attccaggcc	atcgcatgga	gggaagttct	gtgagggctc	1920
cactcgcaat	ctgaagctct	gcaacagtca	gaaatgtccc	cgggacagtg	ttgacttccg	1980
tgtgctcag	tgtgccgagc	acaacagcag	acgattcaga	gggcggcact	acaagtggaa	2040
gcctgatcag	gacttatgca	aactctactg	tatcgagaaa	ggatttgatt	tcttcttttc	2100
tttgtcaaat	aaagtcaaag	atgggactcc	atgctcggag	gatagccgta	atgtttgtat	2160
agatgggata	tgtgagagag	ttggatgtga	caatgtcctt	ggatctgatg	ctgttgaaga	2220
cgtctgtggg	gtgtgtaacg	ggaataaact	agcctgcacg	attcacaggg	gtctctacct	2280
agagtattat	cacatgggtc	ccattccttc	tggagcccg	agtatccgca	tctatgaaat	2340
gaacgtctct	acctcctaca	tttctgtgcg	caatgccctc	agaagggtact	acctgaatgg	2400
gcactggacc	gtggactggc	ccggccggta	caaattttcg	ggcactactt	tcgactacag	2460
acggtcctat	aatgagcccc	agaacttaat	cgctactgga	ccaaccaacg	agacactgat	2520
tgtggagctg	ctgtttcagg	gaaggaaccc	gggtgttgcc	tgggaataact	ccatgcctcg	2580
cttggggacc	gagaagcagc	ccctgcccc	gcccagctac	acttgggcca	tcgtgcgctc	2640
tgagtgtctc	gtgtcctgcg	gagggggtag	gtgccttcca	gtgctgctcc	tggaggcagc	2700
atgtcagcct	ttagccactg	cgtacattgc	actggccttt	cttgaatcct	aatgagcagc	2760
ccggggcttc	tccctgccag	tagcagtgc	attcccaagg	tggggagtg	tggtcctgag	2820
tgtcacttgt	cggcccgagc	tgccttctcc	agtctatctg	cttcagtgtg	tgactctgag	2880
gaagtcagta	gatgcattgc	tt				2902

<210> 6

<211> 856

<212> PRT

<213> Homo sapiens

<400> 6

Met Gly Pro Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro

1

5

10

15

Pro Pro Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr

20

25

30

Val Ser His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala

35

40

45

Val Ser Glu Val Glu Pro Ala Phe Leu Gln Val Cys Arg Ala Arg Glu

50

55

60

Leu Arg Leu Cys Val Glu Ala Phe Pro Ile Ala Asn Ser Gln Pro Gly

65

70

75

80

Phe Leu Asn Leu Ser Asn Val Arg Ser His Trp Arg Glu Gln His Ala

85										90					95				
Ser	Lys	Arg	Ile	Ile	Thr	Asn	Ala	Met	Leu	Gly	Glu	Ser	Ala	Leu	Ala				
			100					105						110					
Ser	Thr	Arg	Lys	Ser	Asn	Cys	Val	Phe	Phe	Leu	Ser	Phe	Tyr	Phe	Phe				
			115				120						125						
Gln	Ser	Gly	Met	Ile	Arg	Thr	Glu	Glu	Ala	Asp	Tyr	Phe	Leu	Arg	Pro				
			130				135					140							
Leu	Pro	Ser	His	Leu	Ser	Trp	Lys	Leu	Gly	Arg	Ala	Ala	Gln	Gly	Ser				
						150				155					160				
Ser	Pro	Ser	His	Val	Leu	Tyr	Lys	Arg	Glu	Val	Leu	Val	Thr	Ser	Arg				
				165					170						175				
Thr	Trp	Glu	Leu	Ala	His	Gln	Pro	Leu	His	Ser	Ser	Asp	Leu	Arg	Leu				
			180					185						190					
Gly	Leu	Pro	Gln	Lys	Gln	His	Phe	Cys	Gly	Arg	Arg	Lys	Lys	Tyr	Met				
			195				200						205						
Pro	Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys				
			210			215					220								
Ser	Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu				
					230					235					240				
Glu	Leu	Asn	Val	Glu	Thr	Leu	Val	Val	Val	Asp	Lys	Lys	Met	Met	Gln				
				245					250					255					
Asn	His	Gly	His	Glu	Asn	Ile	Thr	Thr	Tyr	Val	Leu	Thr	Ile	Leu	Asn				
			260					265						270					
Met	Val	Ser	Ala	Leu	Phe	Lys	Asp	Gly	Thr	Ile	Gly	Gly	Asn	Ile	Asn				
			275				280						285						
Ile	Ala	Ile	Val	Gly	Leu	Ile	Leu	Leu	Glu	Asp	Glu	Gln	Pro	Gly	Leu				
			290			295					300								
Val	Ile	Ser	His	His	Ala	Asp	His	Thr	Leu	Ser	Ser	Phe	Cys	Gln	Trp				
					310					315				320					
Gln	Ser	Gly	Leu	Met	Gly	Lys	Asp	Gly	Thr	Arg	His	Asp	His	Ala	Ile				
				325					330					335					
Leu	Leu	Thr	Gly	Leu	Asp	Ile	Cys	Ser	Trp	Lys	Asn	Glu	Pro	Cys	Asp				
			340					345					350						
Thr	Leu	Gly	Phe	Ala	Pro	Ile	Ser	Gly	Met	Cys	Ser	Lys	Tyr	Arg	Ser				
			355				360					365							
Cys	Thr	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Gly	Leu	Ala	Phe	Thr	Ile	Ala				
			370			375					380								
His	Glu	Ser	Gly	His	Asn	Phe	Gly	Met	Ile	His	Asp	Gly	Glu	Gly	Asn				

385		390		395		400
Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly						
	405			410		415
Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His						
	420			425		430
Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys						
	435			440		445
Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr						
	450			455		460
Gly Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu						
	465			470		475
Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His						
	485			490		495
Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly						
	500			505		510
Thr Ile Cys Gly His Glu His Gly Ala Gly Gly Gln Cys Val Lys Tyr						
	515			520		525
Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser						
	530			535		540
Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His Arg						
	545			550		555
Ser Arg Ser Gln Asn Thr His Ser Arg Pro Ser His Gly Gly Lys Phe						
	565			570		575
Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys						
	580			585		590
Pro Arg Asp Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn						
	595			600		605
Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Asp Gln Asp						
	610			615		620
Leu Cys Lys Leu Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser						
	625			630		635
Leu Ser Asn Lys Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg						
	645			650		655
Asn Val Cys Ile Asp Gly Ile Cys Glu Arg Val Gly Cys Asp Asn Val						
	660			665		670
Leu Gly Ser Asp Ala Val Glu Asp Val Cys Gly Val Cys Asn Gly Asn						
	675			680		685
Asn Ser Ala Cys Thr Ile His Arg Gly Leu Tyr Leu Glu Tyr Tyr His						

690	695	700
Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met		
705	710	715 720
Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr		
	725	730 735
Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe		
	740	745 750
Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn		
	755	760 765
Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu		
	770	775 780
Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg		
785	790	795 800
Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala		
	805	810 815
Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu		
	820	825 830
Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Leu Ala Thr Ala Tyr		
	835	840 845
Ile Ala Leu Ala Phe Leu Glu Ser		
850	855	

<210> 7
 <211> 2895
 <212> DNA
 <213> Homo sapiens

<400> 7
 cgctcctgga tgaagccccg cgcgcgcgga tggcgggggt tggcggcgct gtggatgctg 60
 ttggcgcagg tggccgagca ggtgagtcct gggcgctccc accagcgcgg aaaccgcggg 120
 tccggacagc tggaggcgag tccccgcgg ctcctctccc gcggaccccg ccgtctcacc 180
 gcgatgtcgc cgctgttttc cgcaggcacc tgcgtgcgcc atgggacccg cagcggcagc 240
 gcctgggagc ccgagcgtcc cgcgtctctc tccaccgcgg gagcggccgg gctggatgga 300
 aaagggcggg acatggatga agctggaaac catcgttctc agcaaactaa cacaggaaca 360
 gaaaaccaaa cactgcatgt tctcactcaa tatgacctgg tctctgcta cgaggttgac 420
 cacaggggagc attacgtgtc ccatgaaatc atgcaccatc agcggcggag aagagcagtg 480
 gccgtgtccg aggttgagtc tcttcacctt cggtgaaag gccccaggca cgacttccac 540
 atggatctga ggacttccag cagcctagtg gctcctggct ttattgtgca gacgttggga 600
 aagacaggca ctaagtctgt gcagacttta ccgccagagg acttctgttt ctatcaaggc 660
 tctttgcat cacacagaaa ctgccatcg catggaggga agttctgtga gggctccact 720
 cgcactctga agctctgcaa cagtcagaaa tgtccccggg acagtgttgga cttccgtgct 780
 gctcagtggt ccgagcacia cagcagacga ttcagagggc ggcaactaaa gtggaagcct 840
 tacactcaag tagaagccga cttatgcaaa ctctactgta tcgcagaagg atttgatttc 900
 ttcttttctt tgtcaataaa agtcaaagat gggactccat gctcggagga tagccgtaat 960
 gtttgatatag atgggatatg tgagctcagt gtggtgtcca catctgcgca catgccccag 1020
 ctcaccaagg aagacctctt catcttgcca gatgagtata agtcttgctt acggcataag 1080

cgctctcttc tgaggtccca tagaaatgaa gaactgaacg tggagacctt ggtggtgggc 1140
 gacaaaaaga tgatgcaaaa ccatggccat gaaaatatca ccacctacgt gctcacgata 1200
 ctcaacatgg tatctgcttt attcaaagat ggattgatgg ggaaagatgg gactcgatcat 1260
 gaccacgcca tcttactgac tggctctggat atatgttcct ggaagaatga gccctgtgac 1320
 actttgggat ttgcacccat aagtggaaatg tgtagttaa atcgagctg cactgattat 1380
 gaagatacag gtcttggaact ggccttcacc attgcccattg agtctggaca caactttggc 1440
 atgattcatg atggagaagg gaacatgtgt aaaaagtccg agggcaacat catgtccctt 1500
 acattggcag gacgcaatgg agtcttctcc tggtcaccct gcagccgcca gtatctacac 1560
 aaattttctaa gcaccgctca agctatctgc cttgctgatc agccaaagcc tgtgaaggaa 1620
 tacaagtatc ctgagaaatt gccaggagaa ttatatgatg caaacacaca gtgcaagtgg 1680
 cagttcggag agaaagccaa gctctgcatg ctggacttta aaaaggacat ctgtaaagcc 1740
 ctgtggtgcc atcgatttgg aaggaaatgt gagactaaat ttatgccagc agcagaaggc 1800
 acaatttgtg ggcatgacat gtgtgcccgg ggaggacagt gtgtgaaata tggatgatgaa 1860
 ggccccaagc ccacccatgg cactggtctg gactggtctt cttgggtcccc atgctccagg 1920
 acctgaggag ggggagatc tcataggagt cgctctgca ccaaccccaa gccatcgcat 1980
 ggaggggaagt tctgtgaggg ctccactcgc actctgaagc tctgcaacag tcagaaatgt 2040
 ccccgaggaca gtgttgactt ccgtgctgct cagtgtgccg agcacaacag cagacgattc 2100
 agagggcggc actacaagtg gaagccttac actcaagtag aagatcagga cttatgcaaa 2160
 ctctactgta tcgcagaagg atttgatttc ttcttttctt tgtcaaataa agtcaaagat 2220
 ggactcccat gctcgaggga tagccgtaat gtttgtatag atgggatatg tgagagagtt 2280
 ggatgtgaca atgtccttgg atctgatgct gttgaagacg tctgtggggg gtgtaacggg 2340
 aataactcag cctgcacgat tcacaggggt ctctacacca agcaccacca caccaaccag 2400
 tattatcaca tggtcaccat tccttctgga gcccgagta tccgcatcta tgaaatgaac 2460
 gtctctacct cctacatttc tgtgcgcaat gccctcagaa ggtactacct gaatgggcac 2520
 tggaccgtgg actggcccgg ccggtacaaa ttttcgggca ctactttcga ctacagacgg 2580
 tcctataatg agcccgagaa cttaatcgct actggaccaa ccaacgagac actgattgtg 2640
 gagctgctgt ttcagggaag gaacccgggt gttgcctggg aatactccat gcctcgcttg 2700
 gggaccgaga agcagccccc tgcccagccc agctacactt gggccatcgt gcgctctgag 2760
 tgctccgtgt cctgcggagg gggtaggtgc cttccagtgc tgctcctgga ggcagcatgt 2820
 cagccttcag ccactgcgta cattgcactg gcctttcttg aatcctaata agcagcccgg 2880
 ggcttctccc tgcca 2895

<210> 8
 <211> 952
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
 1 5 10 15
 Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
 20 25 30
 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
 35 40 45
 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
 50 55 60
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
 65 70 75 80
 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 85 90 95

Gly	Lys	Gly	Arg	Asp	Met	Asp	Glu	Ala	Gly	Asn	His	Arg	Ser	Gln	Gln	100	105	110
Thr	Asn	Thr	Gly	Thr	Glu	Asn	Gln	Thr	Leu	His	Val	Leu	Thr	Gln	Tyr	115	120	125
Asp	Leu	Val	Ser	Ala	Tyr	Glu	Val	Asp	His	Arg	Gly	Asp	Tyr	Val	Ser	130	135	140
His	Glu	Ile	Met	His	His	Gln	Arg	Arg	Arg	Arg	Ala	Val	Ala	Val	Ser	145	150	155
Glu	Val	Glu	Ser	Leu	His	Leu	Arg	Leu	Lys	Gly	Pro	Arg	His	Asp	Phe	165	170	175
His	Met	Asp	Leu	Arg	Thr	Ser	Ser	Ser	Leu	Val	Ala	Pro	Gly	Phe	Ile	180	185	190
Val	Gln	Thr	Leu	Gly	Lys	Thr	Gly	Thr	Lys	Ser	Val	Gln	Thr	Leu	Pro	195	200	205
Pro	Glu	Asp	Phe	Cys	Phe	Tyr	Gln	Gly	Ser	Leu	Arg	Ser	His	Arg	Asn	210	215	220
Ser	Pro	Ser	His	Gly	Gly	Lys	Phe	Cys	Glu	Gly	Ser	Thr	Arg	Thr	Leu	225	230	235
Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro	Arg	Asp	Ser	Val	Asp	Phe	Arg	245	250	255
Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	Phe	Arg	Gly	Arg	His	260	265	270
Tyr	Lys	Trp	Lys	Pro	Tyr	Thr	Gln	Val	Glu	Ala	Asp	Leu	Cys	Lys	Leu	275	280	285
Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	Lys	290	295	300
Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	Ile	305	310	315
Asp	Gly	Ile	Cys	Glu	Leu	Ser	Val	Val	Ser	Thr	Ser	Ala	His	Met	Pro	325	330	335
Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys	Ser	340	345	350
Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu	Glu	355	360	365
Leu	Asn	Val	Glu	Thr	Leu	Val	Val	Val	Asp	Lys	Lys	Met	Met	Gln	Asn	370	375	380
His	Gly	His	Glu	Asn	Ile	Thr	Thr	Tyr	Val	Leu	Thr	Ile	Leu	Asn	Met	385	390	395

Val Ser Ala Leu Phe Lys Asp Gly Leu Met Gly Lys Asp Gly Thr Arg
 405 410 415
 His Asp His Ala Ile Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys
 420 425 430
 Asn Glu Pro Cys Asp Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys
 435 440 445
 Ser Lys Tyr Arg Ser Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu
 450 455 460
 Ala Phe Thr Ile Ala His Glu Ser Gly His Asn Phe Gly Met Ile His
 465 470 475 480
 Asp Gly Glu Gly Asn Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser
 485 490 495
 Pro Thr Leu Ala Gly Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser
 500 505 510
 Arg Gln Tyr Leu His Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu
 515 520 525
 Ala Asp Gln Pro Lys Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu
 530 535 540
 Pro Gly Glu Leu Tyr Asp Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly
 545 550 555 560
 Glu Lys Ala Lys Leu Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys
 565 570 575
 Ala Leu Trp Cys His Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met
 580 585 590
 Pro Ala Ala Glu Gly Thr Ile Cys Gly His Asp Met Trp Cys Arg Gly
 595 600 605
 Gly Gln Cys Val Lys Tyr Gly Asp Glu Gly Pro Lys Pro Thr His Gly
 610 615 620
 His Trp Ser Asp Trp Ser Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly
 625 630 635 640
 Gly Gly Val Ser His Arg Ser Arg Leu Cys Thr Asn Pro Lys Pro Ser
 645 650 655
 His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys
 660 665 670
 Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg Ala Ala Gln
 675 680 685
 Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp
 690 695 700

Lys Pro Tyr Thr Gln Val Glu Asp Gln Asp Leu Cys Lys Leu Tyr Cys
705 710 715 720

Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys Val Lys
725 730 735

Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile Asp Gly
740 745 750

Ile Cys Glu Arg Val Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val
755 760 765

Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
770 775 780

His Arg Gly Leu Tyr Thr Lys His His His Thr Asn Gln Tyr Tyr His
785 790 795 800

Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met
805 810 815

Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr
820 825 830

Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe
835 840 845

Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn
850 855 860

Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu
865 870 875 880

Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg
885 890 895

Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala
900 905 910

Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu
915 920 925

Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr
930 935 940

Ile Ala Leu Ala Phe Leu Glu Ser
945 950

<210> 9

<211> 4488

<212> DNA

<213> Homo sapiens

<400> 9

atgtgggctc agtccttct aggaatgttg gccctatcac cagccattgc agaagaactt 60
ccaaactacc tggtagacatt accagccccg ctaaatttcc cctccgttca gaaggtttgt 120

ttggacctga	gccctgggta	cagtgatgtt	aaattcacgg	ttactctgga	gaccaaggac	180
aagacccaga	agttgctaga	atactctgga	ctgaagaaga	ggcacttaca	ttgtatctcc	240
tttcttgtag	cacctcctgc	tggtggcaca	gaagaagtgg	ccacaatccg	ggtgtcggga	300
gttggaata	acatcagctt	tgaggagaag	aaaaaggttc	taattcagag	gcaggggaac	360
ggcacctttg	tacagactga	caaacctctc	tacacccag	ggcagcaagt	gtatttccgc	420
attgtcacca	tggatagcaa	cttcgttcca	gtgaatgaca	agtactccat	ggtggaacta	480
caggatccaa	atagcaacag	gattgcacag	tggctggaag	tggtagctga	gcaaggcatt	540
gtagacctgt	ccttccaact	ggcaccagag	gcaatgctgg	gcacctacac	tgtggcagtg	600
gctgagggca	agacctttgg	tactttcagt	gtggaggaat	atgtgctttc	tccatttctc	660
cttttactct	cttcagtgtc	gccgaagttt	aaggtggaag	tgggtggaacc	caaggagtta	720
tcaacggtgc	aggaatcttt	cttagtaaaa	atttgttgta	ggtacaccta	tggaaagccc	780
atgctagggg	cagtgcaggt	atctgtgtgt	cagaaggcaa	atacttactg	gtatcgagag	840
gtggaacggg	aacagcttcc	tgacaaatgc	aggaaacctct	ctggacagac	tgacaaaaca	900
ggatgtttct	cagcacctgt	ggacatggcc	acctttgacc	tcattggata	tgcgtacagc	960
catcaaata	atattgtggc	tactgttggt	gaggaaggga	caggtgtgga	ggccaatgcc	1020
actcagaata	tctacatttc	tccacaaatg	ggatcaatga	cctttgaaga	caccagcaat	1080
ttttaccatc	caaatttccc	cttcagtggg	aagatgctgc	tcaagtttcc	gcaaggcggg	1140
gtgctccctt	gcaagaacca	tctagtgttt	ctggtgattt	atggcacaaa	tggaaaccttc	1200
aaccagaccc	tggttactga	taacaatggc	ctagctccct	ttaccttgga	gacatccggg	1260
tggaaatggga	cagacgtttc	tctggaggga	aagtttcaaa	tggaaagactt	agtatataat	1320
ccggaacaag	tgccacgtta	ctaccaaata	gcctacctgc	acctgcgacc	cttctacagc	1380
acaacccgca	gcttcccttg	catccaccgg	ctaaacggcc	ccttgaaatg	tggccagccc	1440
caggaagtgc	tgggtggatta	ttacatcgac	ccggccgatg	caagccctga	ccaagagatc	1500
agcttctcct	actatttaat	agggaaagga	agtttggtga	tggaggggca	gaaacacctg	1560
aactctaaga	agaaaggact	gaaagcctcc	ttctctctct	cactgacctt	cacttcgaga	1620
ctggccccctg	atccttccct	ggtgatctat	gccatttttt	ccagtggagg	tgtttagct	1680
gacaaaattc	agttctcagt	cgagatgtgc	tttgacaatc	agcagcttcc	aggagcagaa	1740
gtggagctgc	agctgcaggc	agctcccggg	tccctgtgtg	cgctccgggc	ggtggatgag	1800
agtgtcttac	tgttagggc	agacagagag	ctgagcaacc	gctctgtcta	tgggatgttt	1860
ccattctggt	atggctacta	cccctatcaa	gtggctgagt	atgatcagtg	tccagtgtct	1920
ggcccatggg	actttctca	gccccctc	gacccaatgc	cccaagggca	ttcgagcgct	1980
cgttccatta	tcttgaggcc	ctcgttctct	gaaggcacgg	accttttcag	ctttttccgg	2040
gacgtggggc	tgaataact	gtccaatgcc	aaaatcaaga	agccagtaga	ttgcagtcac	2100
agatctccag	aatacagcac	tgctatgggt	ggcggtggtc	atccagaggc	ttttgagtea	2160
tcaactcctt	tacatcaagc	agaggattct	caggctccgc	agtacttccc	agagacctgg	2220
ctctgggatc	tgtttcctat	tggtaactcg	gggaaggagg	cggtccacgt	cacagttcct	2280
gacgccatca	ccgagtggaa	ggcgatgagt	ttctgcactt	cccagtcaag	aggcttcggg	2340
ctttcaccca	ctggtggact	aactgctttc	aagccgttct	ttgttgacct	gactctccct	2400
tactcagtag	tccgtgggga	atcctttcgt	cttactgcca	ccatcttcaa	ttacctaaag	2460
gattgcatca	gggttcagac	tgacctggct	aaatcgcatg	agtaccagct	agaatcatgg	2520
gcagattctc	agacctccag	ttgtctctgt	gctgatgacg	caaaaaccca	ccactggaac	2580
atcacagctg	tcaaattggg	tcacattaac	tttactatta	gtacaaagat	tctggacagc	2640
aatgaacctat	gtggggggcca	gaaggggttt	gttccccaaa	agggccgaag	tgacacgctc	2700
atcaagccag	ttctcgtcaa	acctgaggga	gtcctggtgg	agaagacaca	cagctcattg	2760
ctgtgcccaa	aaggaggaaa	ggtggcatct	gaactgtctc	cctggagct	cccagtggac	2820
attgttcctg	actcgaccaa	ggcttatgtt	acggttcttg	gagacattat	gggcacagcc	2880
ctgcagaacc	tggatggtct	ggtgcagatg	cccagtggct	gtggcgagca	gaacatggtc	2940
ttgtttgtct	ccatcatcta	tgtcttgag	tacctggaga	aggcagggct	gctgacggag	3000
gagatcaggt	ctcgggcagt	gggtttcctg	gaaatagggt	accagaaggga	gctgatgtac	3060
aaacacagca	atggctcata	cagtgccttt	ggggagcgag	atggaaatgg	aaacacatgg	3120
ctgacagcgt	ttgtcacaaa	atgctttggc	caagctcaga	aattcatctt	cattgatccc	3180
aagaacatcc	aggatgctct	caagtggatg	gcaggaaacc	agctccccag	tggctgctat	3240
gccaacgtgg	gaaatctcct	tcacacagct	atgaagggtg	gtgttgatga	tgaggctctc	3300
ttgactgcgt	atgtcacagc	tgcattgctg	gagatgggaa	aggatgtaga	tgacccaatg	3360
gtgagtcagg	gtctacgggtg	tctcaagaat	tcgccacct	ccacgaccaa	cctctacaca	3420
caggccctgt	tggcttacat	tttctccctg	gctggggaaa	tggacatcag	aaacattctc	3480
cttaaacagt	tagatcaaca	ggctatcatc	tcaggagaat	ccatttactg	gagccagaaa	3540

```

cctactccat catcgaacgc cagcccttgg tctgagcctg cggctgtaga tgtggaactc 3600
acagcatatg cattggttggc ccagcttacc aagcccagcc tgactcaaaa ggagatagcg 3660
aaggccacta gcatagtggc ttggttggcc aagcaacaca atgcatatgg gggcttctct 3720
tctactcagg atactgtagt tgctctccaa gctcttgcca aatatgccac taccgcctac 3780
atgccatctg aggagatcaa cctgggttga aaatccactg agaatttcca gcgcacattc 3840
aacatacagt cagttaacag attggtatct cagcaggata ccctgcccac tgtccctgga 3900
atgtacacgt tggaggcctc aggccagggc tgtgtctatg tgcagacggg gttgagatac 3960
aatattctcc ctcccacaaa tatgaagacc tttagtctta gtgtggaaat agggaaaagct 4020
agatgtgagc aaccgacttc acctcgatcc ttgactctca ctattcacac cagttatgtg 4080
gggagccgta gctcttccaa tatggctatt gtggaagtga agatgctatc tgggttcagt 4140
cccattggagg gcaccaatca gttacttctc cagcaacccc tgggtgaagaa ggttgaattt 4200
ggaactgaca cacttaacat ttacttggat gagctcatta agaacactca gacttacacc 4260
ttcaccatca gccaaagtgt gctggtcacc aacttgaaac cagcaaccat caaggtctat 4320
gactactacc taccaggttc ttttaaatta tctcagtaca caattgtgtg gtccatgaac 4380
aatgacagca tagtggactc tgtggcacgg caccacagaac caccctctt caagacagaa 4440
gcatttattc cttcacttcc tgggagtgtt aacaactgat agctacca 4488

```

```

<210> 10
<211> 1492
<212> PRT
<213> Homo sapiens

```

```

<400> 10
Met Trp Ala Gln Leu Leu Leu Gly Met Leu Ala Leu Ser Pro Ala Ile
  1              5              10              15

Ala Glu Glu Leu Pro Asn Tyr Leu Val Thr Leu Pro Ala Arg Leu Asn
      20              25              30

Phe Pro Ser Val Gln Lys Val Cys Leu Asp Leu Ser Pro Gly Tyr Ser
      35              40              45

Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
      50              55              60

Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
      65              70              75              80

Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
      85              90              95

Arg Val Ser Gly Val Gly Asn Asn Ile Ser Phe Glu Glu Lys Lys Lys
      100             105             110

Val Leu Ile Gln Arg Gln Gly Asn Gly Thr Phe Val Gln Thr Asp Lys
      115             120             125

Pro Leu Tyr Thr Pro Gly Gln Gln Val Tyr Phe Arg Ile Val Thr Met
      130             135             140

Asp Ser Asn Phe Val Pro Val Asn Asp Lys Tyr Ser Met Val Glu Leu
      145             150             155             160

Gln Asp Pro Asn Ser Asn Arg Ile Ala Gln Trp Leu Glu Val Val Pro
      165             170             175

```


Glu Gln Gly Ile Val Asp Leu Ser Phe Gln Leu Ala Pro Glu Ala Met
 180 185 190
 Leu Gly Thr Tyr Thr Val Ala Val Ala Glu Gly Lys Thr Phe Gly Thr
 195 200 205
 Phe Ser Val Glu Glu Tyr Val Leu Ser Pro Phe Leu Leu Leu Leu Ser
 210 215 220
 Ser Val Leu Pro Lys Phe Lys Val Glu Val Val Glu Pro Lys Glu Leu
 225 230 235 240
 Ser Thr Val Gln Glu Ser Phe Leu Val Lys Ile Cys Cys Arg Tyr Thr
 245 250 255
 Tyr Gly Lys Pro Met Leu Gly Ala Val Gln Val Ser Val Cys Gln Lys
 260 265 270
 Ala Asn Thr Tyr Trp Tyr Arg Glu Val Glu Arg Glu Gln Leu Pro Asp
 275 280 285
 Lys Cys Arg Asn Leu Ser Gly Gln Thr Asp Lys Thr Gly Cys Phe Ser
 290 295 300
 Ala Pro Val Asp Met Ala Thr Phe Asp Leu Ile Gly Tyr Ala Tyr Ser
 305 310 315 320
 His Gln Ile Asn Ile Val Ala Thr Val Val Glu Glu Gly Thr Gly Val
 325 330 335
 Glu Ala Asn Ala Thr Gln Asn Ile Tyr Ile Ser Pro Gln Met Gly Ser
 340 345 350
 Met Thr Phe Glu Asp Thr Ser Asn Phe Tyr His Pro Asn Phe Pro Phe
 355 360 365
 Ser Gly Lys Met Leu Leu Lys Phe Pro Gln Gly Gly Val Leu Pro Cys
 370 375 380
 Lys Asn His Leu Val Phe Leu Val Ile Tyr Gly Thr Asn Gly Thr Phe
 385 390 395 400
 Asn Gln Thr Leu Val Thr Asp Asn Asn Gly Leu Ala Pro Phe Thr Leu
 405 410 415
 Glu Thr Ser Gly Trp Asn Gly Thr Asp Val Ser Leu Glu Gly Lys Phe
 420 425 430
 Gln Met Glu Asp Leu Val Tyr Asn Pro Glu Gln Val Pro Arg Tyr Tyr
 435 440 445
 Gln Asn Ala Tyr Leu His Leu Arg Pro Phe Tyr Ser Thr Thr Arg Ser
 450 455 460
 Phe Leu Gly Ile His Arg Leu Asn Gly Pro Leu Lys Cys Gly Gln Pro
 465 470 475 480

Gln Glu Val Leu Val Asp Tyr Tyr Ile Asp Pro Ala Asp Ala Ser Pro
 485 490 495
 Asp Gln Glu Ile Ser Phe Ser Tyr Tyr Leu Ile Gly Lys Gly Ser Leu
 500 505 510
 Val Met Glu Gly Gln Lys His Leu Asn Ser Lys Lys Lys Gly Leu Lys
 515 520 525
 Ala Ser Phe Ser Leu Ser Leu Thr Phe Thr Ser Arg Leu Ala Pro Asp
 530 535 540
 Pro Ser Leu Val Ile Tyr Ala Ile Phe Pro Ser Gly Gly Val Val Ala
 545 550 555 560
 Asp Lys Ile Gln Phe Ser Val Glu Met Cys Phe Asp Asn Gln Gln Leu
 565 570 575
 Pro Gly Ala Glu Val Glu Leu Gln Leu Gln Ala Ala Pro Gly Ser Leu
 580 585 590
 Cys Ala Leu Arg Ala Val Asp Glu Ser Val Leu Leu Leu Arg Pro Asp
 595 600 605
 Arg Glu Leu Ser Asn Arg Ser Val Tyr Gly Met Phe Pro Phe Trp Tyr
 610 615 620
 Gly His Tyr Pro Tyr Gln Val Ala Glu Tyr Asp Gln Cys Pro Val Ser
 625 630 635 640
 Gly Pro Trp Asp Phe Pro Gln Pro Leu Ile Asp Pro Met Pro Gln Gly
 645 650 655
 His Ser Ser Gln Arg Ser Ile Ile Trp Arg Pro Ser Phe Ser Glu Gly
 660 665 670
 Thr Asp Leu Phe Ser Phe Phe Arg Asp Val Gly Leu Lys Ile Leu Ser
 675 680 685
 Asn Ala Lys Ile Lys Lys Pro Val Asp Cys Ser His Arg Ser Pro Glu
 690 695 700
 Tyr Ser Thr Ala Met Gly Gly Gly Gly His Pro Glu Ala Phe Glu Ser
 705 710 715 720
 Ser Thr Pro Leu His Gln Ala Glu Asp Ser Gln Val Arg Gln Tyr Phe
 725 730 735
 Pro Glu Thr Trp Leu Trp Asp Leu Phe Pro Ile Gly Asn Ser Gly Lys
 740 745 750
 Glu Ala Val His Val Thr Val Pro Asp Ala Ile Thr Glu Trp Lys Ala
 755 760 765
 Met Ser Phe Cys Thr Ser Gln Ser Arg Gly Phe Gly Leu Ser Pro Thr
 770 775 780

Val Gly Leu Thr Ala Phe Lys Pro Phe Phe Val Asp Leu Thr Leu Pro
 785 790 795 800
 Tyr Ser Val Val Arg Gly Glu Ser Phe Arg Leu Thr Ala Thr Ile Phe
 805 810 815
 Asn Tyr Leu Lys Asp Cys Ile Arg Val Gln Thr Asp Leu Ala Lys Ser
 820 825 830
 His Glu Tyr Gln Leu Glu Ser Trp Ala Asp Ser Gln Thr Ser Ser Cys
 835 840 845
 Leu Cys Ala Asp Asp Ala Lys Thr His His Trp Asn Ile Thr Ala Val
 850 855 860
 Lys Leu Gly His Ile Asn Phe Thr Ile Ser Thr Lys Ile Leu Asp Ser
 865 870 875 880
 Asn Glu Pro Cys Gly Gly Gln Lys Gly Phe Val Pro Gln Lys Gly Arg
 885 890 895
 Ser Asp Thr Leu Ile Lys Pro Val Leu Val Lys Pro Glu Gly Val Leu
 900 905 910
 Val Glu Lys Thr His Ser Ser Leu Leu Cys Pro Lys Gly Gly Lys Val
 915 920 925
 Ala Ser Glu Ser Val Ser Leu Glu Leu Pro Val Asp Ile Val Pro Asp
 930 935 940
 Ser Thr Lys Ala Tyr Val Thr Val Leu Gly Asp Ile Met Gly Thr Ala
 945 950 955 960
 Leu Gln Asn Leu Asp Gly Leu Val Gln Met Pro Ser Gly Cys Gly Glu
 965 970 975
 Gln Asn Met Val Leu Phe Ala Pro Ile Ile Tyr Val Leu Gln Tyr Leu
 980 985 990
 Glu Lys Ala Gly Leu Leu Thr Glu Glu Ile Arg Ser Arg Ala Val Gly
 995 1000 1005
 Phe Leu Glu Ile Gly Tyr Gln Lys Glu Leu Met Tyr Lys His Ser Asn
 1010 1015 1020
 Gly Ser Tyr Ser Ala Phe Gly Glu Arg Asp Gly Asn Gly Asn Thr Trp
 1025 1030 1035 1040
 Leu Thr Ala Phe Val Thr Lys Cys Phe Gly Gln Ala Gln Lys Phe Ile
 1045 1050 1055
 Phe Ile Asp Pro Lys Asn Ile Gln Asp Ala Leu Lys Trp Met Ala Gly
 1060 1065 1070
 Asn Gln Leu Pro Ser Gly Cys Tyr Ala Asn Val Gly Asn Leu Leu His
 1075 1080 1085

Thr Ala Met Lys Gly Gly Val Asp Asp Glu Val Ser Leu Thr Ala Tyr
 1090 1095 1100

Val Thr Ala Ala Leu Leu Glu Met Gly Lys Asp Val Asp Asp Pro Met
 1105 1110 1115 1120

Val Ser Gln Gly Leu Arg Cys Leu Lys Asn Ser Ala Thr Ser Thr Thr
 1125 1130 1135

Asn Leu Tyr Thr Gln Ala Leu Leu Ala Tyr Ile Phe Ser Leu Ala Gly
 1140 1145 1150

Glu Met Asp Ile Arg Asn Ile Leu Leu Lys Gln Leu Asp Gln Gln Ala
 1155 1160 1165

Ile Ile Ser Gly Glu Ser Ile Tyr Trp Ser Gln Lys Pro Thr Pro Ser
 1170 1175 1180

Ser Asn Ala Ser Pro Trp Ser Glu Pro Ala Ala Val Asp Val Glu Leu
 1185 1190 1195 1200

Thr Ala Tyr Ala Leu Leu Ala Gln Leu Thr Lys Pro Ser Leu Thr Gln
 1205 1210 1215

Lys Glu Ile Ala Lys Ala Thr Ser Ile Val Ala Trp Leu Ala Lys Gln
 1220 1225 1230

His Asn Ala Tyr Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala
 1235 1240 1245

Leu Gln Ala Leu Ala Lys Tyr Ala Thr Thr Ala Tyr Met Pro Ser Glu
 1250 1255 1260

Glu Ile Asn Leu Val Val Lys Ser Thr Glu Asn Phe Gln Arg Thr Phe
 1265 1270 1275 1280

Asn Ile Gln Ser Val Asn Arg Leu Val Phe Gln Gln Asp Thr Leu Pro
 1285 1290 1295

Asn Val Pro Gly Met Tyr Thr Leu Glu Ala Ser Gly Gln Gly Cys Val
 1300 1305 1310

Tyr Val Gln Thr Val Leu Arg Tyr Asn Ile Leu Pro Pro Thr Asn Met
 1315 1320 1325

Lys Thr Phe Ser Leu Ser Val Glu Ile Gly Lys Ala Arg Cys Glu Gln
 1330 1335 1340

Pro Thr Ser Pro Arg Ser Leu Thr Leu Thr Ile His Thr Ser Tyr Val
 1345 1350 1355 1360

Gly Ser Arg Ser Ser Ser Asn Met Ala Ile Val Glu Val Lys Met Leu
 1365 1370 1375

Ser Gly Phe Ser Pro Met Glu Gly Thr Asn Gln Leu Leu Leu Gln Gln
 1380 1385 1390

Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr
 1395 1400 1405

Leu Asp Glu Leu Ile Lys Asn Thr Gln Thr Tyr Thr Phe Thr Ile Ser
 1410 1415 1420

Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr
 1425 1430 1435 1440

Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val
 1445 1450 1455

Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro
 1460 1465 1470

Glu Pro Pro Pro Phe Lys Thr Glu Ala Phe Ile Pro Ser Leu Pro Gly
 1475 1480 1485

Ser Val Asn Asn
 1490

<210> 11
 <211> 987
 <212> DNA
 <213> Homo sapiens

<400> 11
 atgagagcca attgttccag cagctcagcc tgccctgccac acagttcaga ggaggagctg 60
 ccagtgggac tggaggtgca tggaaacctg gagctcgttt tcacagtggg gtccactatc 120
 atgatggggc tgctcatgtt ctctttggga tgttccgtgg agatccggaa gctgtgggtcg 180
 cacatcagga gaccctgggg cattgctgtg ggactgctct gccagtgttg gctcatgcct 240
 ttacagctt atctcctggc cattagcttt tctctgaagc cagtccaagc tattgctgtt 300
 ctcatcatgg gctgctgccg gggggcacca tctctaacat tttcaccttc tgggttgatg 360
 gagatatgga tctcaggtgc cctgggaatg atgccactct gcatttatct ctacacctgg 420
 tcttgagtc ttcagcagaa tctcaccatt ccttatcaga acataggtct gtcttttagga 480
 attacccttg tgtgcctgac cattcctgtg gcctttgggtg tctatgtgaa ttacagatgg 540
 ccaaaacaat ccaaaatcat tctcaaggcc gttgttgggtg gggtcctcct tctgggtgggtc 600
 gcagttgctg gtgtggtcct ggcaaaagga tcttggaatt cagacatcac ccttctgacc 660
 atcagtttca tctttccttt gattggccat gtcacgggtt ttctgctggc actttttacc 720
 caccagtctt ggcaaggac cttgcctatc tttttaggtt tagctttcaa gacaccctgt 780
 gataccctac tcgcaatgac ttcgtgtcct gaatgttcca ggctcatcta tgccttcatt 840
 cctctgctat atggactctt ccagctgata gatggatttc ttattgttga agagagaaca 900
 gaagatacag actgcgatgg ttcaccttta cctgagtatt ttactgaggt aacaataata 960
 cctaaacaac ctaggatatg acagctt 987

<210> 12
 <211> 326
 <212> PRT
 <213> Homo sapiens

<400> 12
 Met Arg Ala Asn Cys Ser Ser Ser Ser Ala Cys Pro Ala Asn Ser Ser
 1 5 10 15

Glu Glu Glu Leu Pro Val Gly Leu Glu Val His Gly Asn Leu Glu Leu

20					25					30					
Val	Phe	Thr	Val	Val	Ser	Thr	Ile	Met	Met	Gly	Leu	Leu	Met	Phe	Ser
35					40					45					
Leu	Gly	Cys	Ser	Val	Glu	Ile	Arg	Lys	Leu	Trp	Ser	His	Ile	Arg	Arg
50					55					60					
Pro	Trp	Gly	Ile	Ala	Val	Gly	Leu	Leu	Cys	Gln	Phe	Gly	Leu	Met	Pro
65					70					75					
Phe	Thr	Ala	Tyr	Leu	Leu	Ala	Ile	Ser	Phe	Ser	Leu	Lys	Pro	Val	Gln
85					90					95					
Ala	Ile	Ala	Val	Leu	Ile	Met	Gly	Cys	Cys	Arg	Gly	Ala	Pro	Ser	Leu
100					105					110					
Thr	Phe	Ser	Pro	Ser	Gly	Leu	Met	Glu	Ile	Trp	Ile	Ser	Gly	Ala	Leu
115					120					125					
Gly	Met	Met	Pro	Leu	Cys	Ile	Tyr	Leu	Tyr	Thr	Trp	Ser	Trp	Ser	Leu
130					135					140					
Gln	Gln	Asn	Leu	Thr	Ile	Pro	Tyr	Gln	Asn	Ile	Gly	Leu	Ser	Leu	Gly
145					150					155					
Ile	Thr	Leu	Val	Cys	Leu	Thr	Ile	Pro	Val	Ala	Phe	Gly	Val	Tyr	Val
165					170					175					
Asn	Tyr	Arg	Trp	Pro	Lys	Gln	Ser	Lys	Ile	Ile	Leu	Lys	Ala	Val	Val
180					185					190					
Gly	Gly	Val	Leu	Leu	Leu	Val	Val	Ala	Val	Ala	Gly	Val	Val	Leu	Ala
195					200					205					
Lys	Gly	Ser	Trp	Asn	Ser	Asp	Ile	Thr	Leu	Leu	Thr	Ile	Ser	Phe	Ile
210					215					220					
Phe	Pro	Leu	Ile	Gly	His	Val	Thr	Gly	Phe	Leu	Leu	Ala	Leu	Phe	Thr
225					230					235					
His	Gln	Ser	Trp	Gln	Arg	Thr	Leu	Pro	Ile	Phe	Leu	Gly	Leu	Ala	Phe
245					250					255					
Lys	Thr	Pro	Cys	Asp	Thr	Leu	Leu	Ala	Met	Thr	Ser	Cys	Pro	Glu	Cys
260					265					270					
Ser	Arg	Leu	Ile	Tyr	Ala	Phe	Ile	Pro	Leu	Leu	Tyr	Gly	Leu	Phe	Gln
275					280					285					
Leu	Ile	Asp	Gly	Phe	Leu	Ile	Val	Glu	Glu	Arg	Thr	Glu	Asp	Thr	Asp
290					295					300					
Cys	Asp	Gly	Ser	Pro	Leu	Pro	Glu	Tyr	Phe	Thr	Glu	Val	Thr	Ile	Ile
305					310					315					
320															
Pro	Lys	Gln	Pro	Arg	Ile										

<210> 13
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 13
 aaaacatggc tgccaaaatg tttgagttca tcggcaagtt tggcctggcc ttagttgttg 60
 caggaggcgt ggtgaactct gccttatata gtgtggatgc tgggcacaga gctgtcgtct 120
 ttgaccgatt ccgtggagtg caggacattg tggtaggcaa agggactcac tgtctcatcc 180
 catggttaca gaaatcaata atctttgact gccgtttctca gccacgtaat gtgccagtca 240
 tcaccggtag caaagattta cagaatgtca acctcacact gcgcatcatc ttccggccccg 300
 tagctagcca gcttcctcac atcttcacca gcagcggaga ggaccatgat gagcgtgtgc 360
 cgccgtccat cacgaacaag atcctcaagt cagtgggtggc tcgctttgaa gctggagAAC 420
 taatcaccca gagagagcag atctccaggc aggtgagcga tgaccttacg gagccagcag 480
 ccacctttgg gctcattctg gacgacgtgt ccttgacata tctgaccttc ggggaaggagt 540
 tcatagaagc ggtggaagcc aaacagatag ctccagcagga agcagagagg gccagatttg 600
 tgggtggaaaa ggctgagcag cagaaaaagg cggccatcat ttctgctgag ggcgactcca 660
 aggtggccga gctgatcacc aactcactgg ccacagcagg ggacgccctg atcgagctgc 720
 gcaagctgga agctgtggag gacatcacct accagctttt acgctctcgg aacatcacct 780
 acctgcgggc agggcagtc atgcccctgc agctgcgctg gtgagggccc acctgcctg 840
 cacctccgag 850

<210> 14
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Ala Ala Lys Met Phe Glu Phe Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Val Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Ser Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Val Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Lys Gly Thr His Cys Leu Ile Pro Trp Leu Gln Lys Ser
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Gln Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Leu Thr Leu Arg Ile Ile Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro His Ile Phe Thr Ser Ser Gly Glu
 100 105 110
 Asp His Asp Glu Arg Val Pro Pro Ser Ile Thr Asn Lys Ile Leu Lys
 115 120 125
 Ser Val Val Ala Arg Phe Glu Ala Gly Glu Leu Ile Thr Gln Arg Glu

130	135	140
Gln Ile Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Pro Ala Ala Thr		
145	150	155 160
Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr Leu Thr Phe Gly		
	165	170 175
Lys Glu Phe Ile Glu Ala Val Glu Ala Lys Gln Ile Ala Gln Gln Glu		
	180	185 190
Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys		
	195	200 205
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Val Ala Glu Leu Ile		
	210	215 220
Thr Asn Ser Leu Ala Thr Ala Gly Asp Ala Leu Ile Glu Leu Arg Lys		
225	230	235 240
Leu Glu Ala Val Glu Asp Ile Thr Tyr Gln Leu Leu Arg Ser Arg Asn		
	245	250 255
Ile Thr Tyr Leu Arg Ala Gly Gln Ser Met Pro Leu Gln Leu Arg Trp		
	260	265 270

<210> 15

<211> 2011

<212> DNA

<213> Homo sapiens

<400> 15

```

atggggtggc tccactcct gctgcttctg actcaatgct taggggtccc tggtcagcgc 60
tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct gctacatgcg 120
gtggtgcccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc tggtcgctgt 180
gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg ttgccaaactg 240
ctgccatgga ctcaaacactc gccccacacg aggetgcggc gttctgggcg ctgtgacctc 300
ttccagaaga aagactacgt acggacctgc atcatgaaca atggggttgg gtaccggggc 360
accatggcca cgaccgtggg tggcctgccc tgccaggcctt ggagccacaa gttcccaaat 420
gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg ccgtaaccct 480
gatggcgacc ccggagggtcc ctggtgctac acaacagacc ctgctgtgcg cttccagagc 540
tgcggcacatca aatcctgccc ggaggccgcg tgtgtctggt gcaatggcga ggaataccgc 600
ggcgcggtag accgcacgga gtcaggggcg gagtgccagc gctgggatct tcagcaccgc 660
caccagcacc ccttcgagcc gggcaagttc ctgcaccaag gtctggacga caactattgc 720
cggaatcctg acggctccga gcgccatgg tctacacta cggatccgca gatcgagcga 780
gagttctgtg acctcccccg ctgcggttcc gaggcacagc cccgccaaga ggccacaact 840
gtcagctgct tccgcgggaa gggtgagggc taccggggca cagccaatac caccaccgcg 900
ggcgtacctt gccagcgttg ggacgcgcaa atcccgcac agcaccgatt tacgccagaa 960
aaatacgctg gcaaggacct tcgggagaac ttctgccgga accccgacgg ctgagaggcg 1020
ccctggtgct tcacactgcg gcccggcatg cgcgcggcct tttgctacca gatccggcgt 1080
tgtacagacg acgtgcggcc ccagactgct accacggcgc aggggagcag taccgcggca 1140
cggtcagcaa gacccgcaag ggtgtccagt gccagcgtg gtccgctgag acgccgcaca 1200
agccgcagtt cacgtttacc tccgaaccgc atgcacaact ggaggagaac ttctgccgga 1260

```



```

accagatgg ggatagccat gggccctggt gctacacgat ggacccaagg accccattcg 1320
actactgtgc cctgcgacgc tgcgctgatg accagccgcc atcaatcctg gacccccag 1380
accaggtgca gtttgagaag tgtggcaaga ggggtgatcg gctggatcag cggcggtcca 1440
agctgcgcgt ggttgggggc catccgggca actcacctg gacagtcagc ttgcggaatc 1500
ggtatgtgc ctctcacggg ctatgaggta tggttgggca ccctgttcca gaaccacag 1560
catggagagc caagcctaca gcgggtccca gtagccaaga tgggtgtgtgg gccctcaggc 1620
tcccagcttg tcctgctcaa gctggagaga tctgtgaccc tgaaccagcg tgtggccctg 1680
atctgcctgc cccctgaatg gtatgtggtg cctccaggga ccaagtgtga gattgcaggc 1740
tggggtgaga ccaaaggtac gggtaatgac acagtcctaa atgtggcctt gctgaatgtc 1800
atctccaacc aggagtgtaa catcaagcac cgaggacgtg gtgactacgg gggcccactt 1860
gcctgcttta cccacaactg ctgggtcctg gaaggaatta taatcccaa ccgagtatgc 1920
gcaaggtcct gctggccagc tgtcttcacg cgtgtctctg tgtttgtgga ctggattcac 1980
aaggtcatga gactgggtta ggcccagcct t 2011

```

<210> 16

<211> 666

<212> PRT

<213> Homo sapiens

<400> 16

```

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
  1                      5                      10                      15

```

```

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
      20                      25                      30

```

```

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
      35                      40                      45

```

```

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
      50                      55                      60

```

```

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
      65                      70                      75                      80

```

```

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
      85                      90                      95

```

```

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
      100                      105                      110

```

```

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
      115                      120                      125

```

```

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
      130                      135                      140

```

```

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
      145                      150                      155                      160

```

```

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
      165                      170                      175

```

```

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
      180                      185                      190

```

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
 195 200 205
 Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
 210 215 220
 Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
 225 230 235 240
 Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
 245 250 255
 Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
 260 265 270
 Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
 275 280 285
 Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Thr Ala Thr Thr Ala Gln Gly Ser Ser Thr Ala Ala Arg Ser Ala Arg
 370 375 380
 Pro Ala Arg Val Ser Ser Ala Ser Ala Gly Pro Leu Arg Arg Arg Thr
 385 390 395 400
 Ser Arg Ser Ser Arg Leu Pro Pro Asn Arg Met His Asn Trp Arg Arg
 405 410 415
 Thr Ser Ala Gly Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala Thr
 420 425 430
 Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala Ala
 435 440 445
 Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys Ser
 450 455 460
 Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Gly Val Pro
 465 470 475 480
 Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln Ser
 485 490 495

Ala Cys Gly Ile Gly Met Leu Pro Leu Thr Gly Tyr Glu Val Trp Leu
500 505 510

Gly Thr Leu Phe Gln Asn Pro Gln His Gly Glu Pro Ser Leu Gln Arg
515 520 525

Val Pro Val Ala Lys Met Val Cys Gly Pro Ser Gly Ser Gln Leu Val
530 535 540

Leu Leu Lys Leu Glu Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu
545 550 555 560

Ile Cys Leu Pro Pro Glu Trp Tyr Val Val Pro Pro Gly Thr Lys Cys
565 570 575

Glu Ile Ala Gly Trp Gly Glu Thr Lys Gly Thr Gly Asn Asp Thr Val
580 585 590

Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile
595 600 605

Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr
610 615 620

His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys
625 630 635 640

Ala Arg Ser Cys Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val
645 650 655

Asp Trp Ile His Lys Val Met Arg Leu Gly
660 665

<210> 17
<211> 634
<212> DNA
<213> Homo sapiens

<400> 17
caagctgccc acgccgacgg caaccctgct ctgcatgccc gcccgcccgt gccaccatg 60
gccacagttc agcagctggg aggaagatgg cgccctggtg acagcaaacg ctttgatgaa 120
tacatgaagg agggaggagt gggaaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180
gattgtatca tcacttgtga tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240
acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300
actcagactg tgtgcagctt tgcagatggt gcattgggtc agcatcagga gtgggatggg 360
aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtggtgta ctgtgtcatg 420
aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatacttt 480
ggacaggagt taactaatag aatgatcaag ctacagttcaa tgagcaaate tccatagtgt 540
tttttttcat tactgtgttc aattatcttt atcacaaaacg tttcacatgc agctatttca 600
aagtgtcttg gattaattag gatcatccct ttgg 634

<210> 18
<211> 134
<212> PRT
<213> Homo sapiens

<400> 18

Met Ala Thr Val Gln Gln Leu Gly Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15

Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu
20 25 30

Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe
50 55 60

Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg
65 70 75 80

Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His
85 90 95

Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp
100 105 110

Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg
115 120 125

Ile Tyr Glu Lys Val Glu
130

<210> 19

<211> 822

<212> DNA

<213> Homo sapiens

<400> 19

catgaactgg gcatttctgc agggcctgct gagtggcgtg aacaagtact ccacagtgct 60
gagccgcattc tggctgtctg tgggtgttcat ctttcgtgtg ctgggtgtacg tgggtggcagc 120
ggaggagggtg tgggacgatg agcagaagga ctttgtctgc aacaccaagc agcccggctg 180
ccccaacgtc tgctatgacg agttcttccc cgtgtcccac gtgcgcctct gggccctaca 240
gtcctactctg gtcacgtgcc cctcactgct cgtgggtcatg cactggcct accgcgagga 300
acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360
gagcaagaag cggggcggac tgtggtggac gtacttgctg agcctcatct tcaaggccgc 420
cgtggatgct ggcttctct atattctcca ccgcctctac aaggattatg acatgccccg 480
cgtgggtggc tgctccgtgg agccttgccc ccacactgtg gactggtaca tctcccggcc 540
cagggagaag aaggtcttca cctacttcat ggtgaccaca gctgccatct gcatcctgct 600
caacctcagt gaagtcttct acctggtggg caagagggtgc atggagatct tcggccccag 660
gcaccggcgg cctcggtgcc gggaatgcct acccgatacg tgcccaccat atgtcctctc 720
ccaggagggg caccctgagg atgggaactc tgtcctaata aaggctgggt cggccccagt 780
ggatgcaggt gggtatccat aacctgcgag atcagcagat aa 822

<210> 20

<211> 266

<212> PRT

<213> Homo sapiens

<400> 20

Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15
Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
20 25 30
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
35 40 45
Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95
Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
100 105 110
Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
130 135 140
Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160
Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175
Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
180 185 190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
195 200 205
Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
210 215 220
Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
225 230 235 240
Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
245 250 255
Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
260 265

<210> 21

<211> 546

<212> DNA

<213> Homo sapiens

```

<400> 21
caatctgaca tgtaactgta aaatcactgg gcccgaggag tgactgtaat taagggctta 60
cggttgaaaat gtataaacag agcttgattc ttaagtctcg aaaattcttc acagtgatgg 120
tgtgaactaa atccacagcc acataataat caaacacagaa aagcaaaaaga aagccacttc 180
aggaaatacc acggtcacac ctcagttggc ttcattgctac agattataga aaatatgttg 240
ctgcccgggc caccaatctg ttggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300
gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360
agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420
cttttagtac tgacattctg gattttaaaa gttatgttga ccgcatgttc tcaactcaca 480
gtgggagttg aacaatgaga acacacggac acggggaagg gaacatcaca caccagggcc 540
tgtcag
546

```

```

<210> 22
<211> 61
<212> PRT
<213> Homo sapiens

```

```

<400> 22
Met Leu Gln Ile Ile Glu Asn Met Leu Leu Pro Gly Pro Pro Ile Cys
  1             5             10             15

Trp Phe Thr Leu Leu Arg Glu Gln Cys Lys Cys Leu Gln Glu Ala Ile
      20             25             30

His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val
      35             40             45

Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser
      50             55             60

```

```

<210> 23
<211> 2309
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (2196)
<223> Wherein n is an a o t o r c o r g.

```

```

<400> 23
gagtgaagg tcggacagac tgtggagccg acagactgaa ggacagcggc accgccagac 60
ggccagaaaag ttccgccatg agctggggca cggagctgtg ggatcagttc gacagcttag 120
acaagcatac acaatgggga attgacttct tggaaagata tgccaaattt gttaaagaga 180
ggatagaaat tgaacagaac tatgcgaaac aattgagaaa tctggttaag aagtactgcc 240
ccaaacgttc atccaaagat gaagagccac gggttacctc gtgtgtagcc ttttttaata 300
tccttaatga gttaaattgac tatgcaggac agcgagaagt tgtagcagaa gaaatggcgc 360
acagagtgtg ttggtgaatta atgagatatg ctcatgatct gaaaactgaa agaaaaatgc 420
atctgcaaga aggacgaaaa gctcaacaat atcttgacat gtgctggaaa cagatgggta 480
atagtaaaaa gaagtttgaa agagaatgta gagaggcaga aaaggcacaa cagagttatg 540
aaagattgga taatgatact aatgcaacca aggcagatgt tgaaaatgcc aaacagcagt 600
tgaatctgcg tacgcatatg gccgatgaaa ataaaaatgc atatgctgca caattacaaa 660
actttaatgg agaacaacat aaacattttt atgtagtgtat tcctcagatt tacaagcaac 720
tacaagaaat ggacgaacga aggactatta aactcagtga gtgttacaga ggatttgctg 780

```

```

actcagaacg caaagttatt cccatcattt caaaatgttt ggaaggaatg attcttgcag 840
caaaatcagt tgatgaaaga agagactctc aaatggtggt agactccttc aaatctgggt 900
ttgaacctcc aggagacttt ccatttgaag attacagtca acatatatat agaaccattt 960
ctgatgggac tatcagtgca tccaaacagg agagtgggaa gatggatgcc aaaaccccag 1020
taggaaaaggc caagggcaaa ttgtggctct ttggaaaagaa gccaaagggc ccagcactag 1080
aagatttcag tcatctgcca ccagaacaga gacgtaaaaa actacagcag cgcattgatg 1140
aacttaacag agaactacag aaagaatcag accaaaaaga tgcactcaac aaaatgaaag 1200
atgtatatga gaaggatcca caaatggggg atccaggggg tttgcagcct aaattagcag 1260
agaccatgaa taacattgac cgcctacgaa tggaaatcca taagaatgag gcttggctct 1320
ctgaagtcga aggcaaaaca ggtgggagag gagacagaag acatagcagt gacataaatc 1380
atcttgtaac acagggacga gaaagtcttg agggaagtta cactgatgat gcaaaccagg 1440
aagtccgtgg gccaccccag cagcatggtc accacaatga gtttgatgat gaatttgagg 1500
atgatgatcc cttgcctgct attggacact gcaaagctat ctaccctttt gatggacata 1560
atgaaggtac tctagcaatg aaagaaggtg aagttctcta cattatagag gaggacaaag 1620
gtgacggatg gacaagagct cggagacaga acggtgaaga aggtacgtt cccacgtcat 1680
acatagatgt aactctagag aaaaacagta aaggttcctg aagaggggtt ctgaggaaat 1740
gggcaagatg ttgaaggagg ttacatgcag ctgcttttgg gggaggggtat tagagttgtc 1800
aggctcaaag agagtgagag aagcaagttg catgagtgca tgcagacatg attttttttt 1860
tactaacttc attagcattt ccatacattg tttttaaaaa tcataatacc aacctttaag 1920
ttcctagttc acagttattc ccacaaaaga aaaagccaac aatagtgtac cttttttcta 1980
ttttatttta ttgctgtcta atcaataaag aatgcagagc tgtcaaaaaa tgtgtcttac 2040
atntagctgt cccaacagga ttgtcttccc tcccagctct ggttttaatt ggcttttaga 2100
cccactatct gtcagatcct tgccatctgt cagtgtctgc ctgcgccacc tccgtgcttg 2160
cctaacatcc tgttgcatgt ctagcgtgat tgagcnagat tttcaggcat gtcttttagaa 2220
tcccctggtn ctgtcaaagc ctggtttggt ttacattggt ngtgcaatcn ctttgtcaac 2280
atctccagca ctatngttcc ntcttaggt 2309

```

<210> 24

<211> 547

<212> PRT

<213> Homo sapiens

<400> 24

```

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Ser Leu Asp Lys
  1                      5                      10                      15

His Thr Gln Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val
      20                      25                      30

Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn
      35                      40                      45

Leu Val Lys Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro
      50                      55                      60

Arg Phe Thr Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn
      65                      70                      75                      80

Asp Tyr Ala Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg
      85                      90                      95

Val Tyr Gly Glu Leu Met Arg Tyr Ala His Asp Leu Lys Thr Glu Arg
      100                      105                      110

Lys Met His Leu Gln Glu Gly Arg Lys Ala Gln Gln Tyr Leu Asp Met
      115                      120                      125

```

Cys Trp Lys Gln Met Gly Asn Ser Lys Lys Lys Phe Glu Arg Glu Cys
 130 135 140
 Arg Glu Ala Glu Lys Ala Gln Gln Ser Tyr Glu Arg Leu Asp Asn Asp
 145 150 155 160
 Thr Asn Ala Thr Lys Ala Asp Val Glu Asn Ala Lys Gln Gln Leu Asn
 165 170 175
 Leu Arg Thr His Met Ala Asp Glu Asn Lys Asn Ala Tyr Ala Ala Gln
 180 185 190
 Leu Gln Asn Phe Asn Gly Glu Gln His Lys His Phe Tyr Val Val Ile
 195 200 205
 Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met Asp Glu Arg Arg Thr Ile
 210 215 220
 Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val
 225 230 235 240
 Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys
 245 250 255
 Ser Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys
 260 265 270
 Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln
 275 280 285
 His Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser Lys Gln
 290 295 300
 Glu Ser Gly Lys Met Asp Ala Lys Thr Pro Val Gly Lys Ala Lys Gly
 305 310 315 320
 Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys Gly Pro Ala Leu Glu Asp
 325 330 335
 Phe Ser His Leu Pro Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg
 340 345 350
 Ile Asp Glu Leu Asn Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp
 355 360 365
 Ala Leu Asn Lys Met Lys Asp Val Tyr Glu Lys Asp Pro Gln Met Gly
 370 375 380
 Asp Pro Gly Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile
 385 390 395 400
 Asp Arg Leu Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu
 405 410 415
 Val Glu Gly Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp
 420 425 430

Ile Asn His Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr
 435 440 445

Thr Asp Asp Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly
 450 455 460

His His Asn Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro
 465 470 475 480

Ala Ile Gly His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu
 485 490 495

Gly Thr Leu Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu
 500 505 510

Asp Lys Gly Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu
 515 520 525

Gly Tyr Val Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser
 530 535 540

Lys Gly Ser
 545

<210> 25
 <211> 1787
 <212> DNA
 <213> Homo sapiens

<400> 25
 gcggaacatt gcctagtaga ccctgaggct ttacaacagt gccactgacc cctatgagcc 60
 tgatgctgga tgaccaaccc cctatggagg cccagtatgc agaggagggc ccaggacctg 120
 ggatcttcag agcagagcct ggagaccagc agcatcccat ttctcaggcg gtgtgctggc 180
 gttccatgcg acgtggctgt gcagtgtctg gagccctggg gctgctggcc ggtgcagggtg 240
 ttggctcatg gctcctagt ctgtatctgt gtctgctgc ctctcagccc atttccggga 300
 ccttgagga tgaggagata actttgagct gctcagaggc cagcgtgag gaagctctgc 360
 tccctgcact tcccaaaaca gtatctttca gaataaacag cgaagacttc ttgctggaag 420
 cgcaagttag ggatcagcca cgctggctcc tgggtctgcca tgagggtctg agccccgcc 480
 tggggctgca gatctgtctg agccttgggc atctcagact cactcaccac aaggagtaa 540
 acctactga catcaaacct aacagttccc aggagtttgc tcagctctct cctagactgg 600
 gaggttctt ggaggaggcg tggcagccca gtaggactac tgaggctgtt aggaacaact 660
 gcacttctgg tcaagtgtt tccctcagat gctctgagtg tggagcgagg cccctggctt 720
 cccgatagt tgggtggcag tctgtggctc ctgggcgctg gccgtggcag gccagcgtg 780
 ccttgggctt ccggcacacg tgtgggggct ctgtgctagc gccacgctgg gtggtgactg 840
 ctgcacattg tatgcacagt ttcaggctgg cccgcctgtc cagctggcgg gttcatgcgg 900
 ggctggctcag ccacagtgcc gtcaggcccc accaaggggc tctgggtggag aggattatcc 960
 cacacccct ctacagtgcc cagaatcatg actacgagc cgcctcctg aggtccaga 1020
 ccgctctcaa cttctcagac actgtgggct ctgtgtgct gccggccaag gaacagcatt 1080
 ttccgaagg ctcgcggtgc tgggtgtctg gctggggcca caccaccct agccatactt 1140
 acagctcgga tatgtccag gacacgggtg tgccccctgt cagcactcag ctctgcaaca 1200
 gctcttgct gtacagcga gccctcacc cccgcctgct ttgcgctggc tacctggacg 1260
 gaagggctga tgcagtcag ggagatagcg ggggccccct agtgtgcca gatggggaca 1320
 catggcgct agtgggggtg gtcagctggg ggcgtggtg cgcagagccc aatcaccag 1380
 gtgtctacgc caagtagct gagtttctg actggatcca tgacactgct caggtgagtg 1440
 tgggggcagg agtagggcag ggagatttct aaaggacctg ccctcgaatg caaggaacct 1500

```

tacccttag gcccgggccc tgctggggac tggggaggggt gctaggacat attccccaga 1560
gtgagtggag gaagaagtga agcttaaaca tggaatccat tggatttcta tcagtttaag 1620
gatgaactgg gtaagagtat gcctgagttt gtatcccaga tctaccattt cctgtgtcga 1680
cctttggcaa atttctaact ttgttaaacc ttaatttcct gataataacc atgatggcta 1740
cttatatgct attgttatat gctattaaat aagacccgta caatgcc 1787

```

```

<210> 26
<211> 1787
<212> DNA
<213> Homo sapiens

```

```

<400> 26
ggcattgtac gggctcttatt taatagcata taacaatagc atataagtag ccatcatggg 60
tattatcagg aaattaaggt ttaacaaagt tagaaatttg ccaaagggtcg acacaggaaa 120
tggtagatct gggatacaaa ctcaggcata ctcttaccga gttcatcctt aaactgatag 180
aaatccaatg gattccatgt ttaagcttca ctcttcctc cactcactct ggggaatatg 240
tcctagcacc ctccccagtc ccacgacagg cccgggccta aggggtaagg ttccctgcat 300
tcgagggcag gtcctttaga aatctccctg ccctactcct gccccacac tcacctgagc 360
agtgtcatgg atccagtcca gaaactcagc taccttggcg tagacacctg ggtgattggg 420
ctctgcgcag ccacgcccc agctgaccac cccactagg cgccatgtgt ccccatctgg 480
gcacactagg gggccccgcg tatctccctg gcatgcatca gcccttcctg ccaggtagcc 540
agcgcaaagc atgcgggggg tgagggctcc gctgtacacg caagagctgt tgcagagctg 600
agtgtcagc aggggcacca ccgtgtcctg gagcatatcc gagctgtaag tatggctagg 660
gtgggtgtgg cccagccag acacccagca ccgcgagccc ttcggaaaat gctgttcctt 720
ggccggcagg cacacagcgc ccacagtgtc tgagaagttg agagcgggtc ggagcctcag 780
gagggcgacg tcgtagtcat gattctgggc actgtagagg ggggtgtggg taatcctctc 840
caccagagcc ccttgggtgg gcctgacggc actgtggctg accagccccg catgaacccg 900
ccagctggac aggcggggcca gcctgaaact gtgcatacaa tgtgcagcag tcaccacca 960
gcgtggcgct agcacagagc cccacacgt gtgcccgaag cccagggcca cgctggcctg 1020
ccacggccag cgcccaggag ccacagactg cccaccaact atccgggaag ccaggggcct 1080
cgctccacac tcagagcatc tgagggaaac aacttgacca gaagtgcagt tgttcctaac 1140
agcctcagta gtcctactgg gctgccacgc ctctccagg aagcctccca gtctaggaga 1200
gagctgagca aactcctggg aactgttgag tttgatgtca gtgaggttta ctcccttggtg 1260
gtgagtgagt ctgagatgcc caaggctcca gcagatctgc agccccaggg cggggctcca 1320
gccctcatgg cagaccagga gccagcgtgg ctgatccctc acttgcgctt ccagcaagaa 1380
gtcttcgctg tttattctga aagatactgt tttgggaagt gcagggagca gagcttcctc 1440
agcgtcggcc tctgagcagc tcaaagttat ctctcatcc tgcaagggtc cggaatggg 1500
ctgagaggca gcaggacaca gatacagcac taggagccat gagccaacac ctgcaccggc 1560
cagcagcccc agggctccca gcaactgcaca gccacgtcgc atggaacgcc agcacaccgc 1620
ctgagaaatg gtagtctgct ggtctccagg ctctgctctg aagatcccag gtcctggggc 1680
ctcctctgca tactgggcct ccataggggg ttggtcatcc agcatcaggc tcataggggt 1740
cagtggcact gttgtaaagc ctcaggggtc actaggcaat gttccgc 1787

```

```

<210> 27
<211> 472
<212> PRT
<213> Homo sapiens

```

```

<400> 27
Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
  1              5              10              15
Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
      20              25              30

```

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Ser Arg Thr Thr Glu Ala Val Arg Asn Asn Cys Thr Ser Gly Gln Val
 195 200 205
 Val Ser Leu Arg Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg
 210 215 220
 Ile Val Gly Gly Gln Ser Val Ala Pro Gly Arg Trp Pro Trp Gln Ala
 225 230 235 240
 Ser Val Ala Leu Gly Phe Arg His Thr Cys Gly Gly Ser Val Leu Ala
 245 250 255
 Pro Arg Trp Val Val Thr Ala Ala His Cys Met His Ser Phe Arg Leu
 260 265 270
 Ala Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Ser
 275 280 285
 Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro His
 290 295 300
 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Arg
 305 310 315 320
 Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu
 325 330 335

Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val Ser
 340 345 350

Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met Leu
 355 360 365

Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn Ser Ser
 370 375 380

Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr
 385 390 395 400

Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
 405 410 415

Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser Trp
 420 425 430

Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys Val
 435 440 445

Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Val Ser Val Gly
 450 455 460

Ala Gly Val Gly Gln Gly Asp Phe
 465 470

<210> 28

<211> 2148

<212> DNA

<213> Homo sapiens

<400> 28

```

acgcgggata cagggagggg ccatgtgcga accagggaga cctcatcttc caaccaagct 60
tgctgggctt gcatttaatc aatgcatggc cagagaacag gagecggaaca ttgcctagta 120
gacctgagg ctttacaaca gtgctactga cccctatgag cctgatgctg gatgaccaac 180
cccctatgga ggcccagtat gcagaggagg gcccaggacc tgggatcttc agagcagagc 240
ctggagacca gcagcatccc atttctcagg cgggtgtgctg gcgttccatg cgacgtggct 300
gtgcagtgtc gggagccctg gggctgctgg ccggtgcagg tgttggctca tggctcctag 360
tgctgtatct gtgtcctgct gcctctcagc ccatctccgg gaccttgagc gatgaggaga 420
taactttgag ctgctcagag gccagcgctg aggaagctct gctccctgca ctccccaaaa 480
cagtatcttt cagaataaac agcgaagact tcttgctgga agcgcaagtg agggatcagc 540
cacgctggct cctggtctgc catgagggct ggagccccgc cctggggctg cagatctgct 600
ggagccttgg gcatctcaga ctcactcacc acaaggagtg aaacctcact gacatcaaac 660
tcaacagttc ccaggagtgt gctcagctct ctccctagact gggaggcttc ctggaggagg 720
cgtggcagcc caggaacaac tgcacttctg gtcaagttgt ttccctcaga tgctctgagt 780
gtggagcgag gccctggct tcccggatag ttggtgggca gtctgtggct cctgggcgct 840
ggcctgggca ggccagcgtg gccctgggct tccggcacac gtgtgggggc tctgtgctag 900
cgccacgctg ggtggtgact gctgcacatt gtatgcacag tgcccagaat catgactacg 960
acgtcgccct cctgaggctc cagaccgctc tcaacttctc agacactgtg ggcgctgtgt 1020
gcctgccggc caaggaacag cattttccga agggctcgcg gtgctgggtg tccggctggt 1080
gccacacca ccctagccat acttacagct cggatatgct ccaggacacg gtggtgcccc 1140
tgctcagcac tcagctctgc aacagctctt gcgtgtacag cggagccctc accccccgca 1200
tgctttgcgc tggctacctg gacggaaggg ctgatgcatg ccaggagat agcgggggcc 1260
ccctagtgtg ccagatggg gacacatggc gcctagtggg ggtggtcagc tgggggcgtg 1320
gctgcgcaga gccaatcac ccagggtgtc acgccaaggt agctgagttt ctggactgga 1380

```

```

tccatgacac tgctcaggac tccctcctct gagtcctgct gtttcctcca gtctcactgc 1440
acaccactgc ctcatgcttc ctggggcctc cagcagctcc actaatggag gagaggcagt 1500
agcctccgac acagaacgca tggacctcct actactgtgt gtgaggaaca gtcactacc 1550
actggccagc caccagcca acaggtctct cctcttgggc cctgatttca gagtcctctt 1620
tctcactaga gactcaatga cagaagagag gctgggactt ggttgggcat gctgtggttg 1680
ctgagggatg agggggagga gagaggtagg agctggagat gaagagactg ctagaagcag 1740
caggaagcct gcccttctgc cctctccctt ccttggcctt gtgtgagtct tttagggagg 1800
gtgactggga ggtgcccccc gtccccactt tttcctgtgc tctaggtggg ctaagtgcct 1860
ccctagagga ctccatggct gagaggctcc tgggcagatg gggtaaggc tgggccagtc 1920
ccagatgaag cctatgggag tcaggaccct ctccactctc cctctccact ccccttctctg 1980
ttctcacctg gctgtggctg gccctgtgtg gggtaggtac actggaaaac aagaagggtt 2040
gagttggtct aggacattgg ttttaaatga cagttctgtg aactggtcca aggaggttct 2100
gttattaaag tgatatatgg tcttgaaaaa aaaaaaaaaa aaaaaaaaaa 2148

```

<210> 29

<211> 418

<212> PRT

<213> Homo sapiens

<400> 29

```

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
  1              5              10              15

```

```

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
      20              25              30

```

```

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
      35              40              45

```

```

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
      50              55              60

```

```

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
      65              70              75              80

```

```

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
      85              90              95

```

```

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
      100             105             110

```

```

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
      115             120             125

```

```

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
      130             135             140

```

```

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
      145             150             155             160

```

```

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
      165             170             175

```

```

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
      180             185             190

```

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205
 Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220
 Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240
 His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255
 Ala His Cys Met His Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu
 260 265 270
 Leu Arg Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val
 275 280 285
 Cys Leu Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp
 290 295 300
 Val Ser Gly Trp Cys His Thr His Pro Ser His Thr Tyr Ser Ser Asp
 305 310 315 320
 Met Leu Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn
 325 330 335
 Ser Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala
 340 345 350
 Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly
 355 360 365
 Pro Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val
 370 375 380
 Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala
 385 390 395 400
 Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser
 405 410 415
 Leu Leu

<210> 30
 <211> 1593
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
 1 5 10 15
 Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
 20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
 35 40 45
 Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
 50 55 60
 His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
 65 70 75 80
 Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
 85 90 95
 His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
 100 105 110
 Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
 115 120 125
 Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
 130 135 140
 Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
 145 150 155 160
 His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile
 165 170 175
 Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His
 180 185 190
 Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys
 195 200 205
 Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg
 210 215 220
 Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg
 225 230 235 240
 Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr
 245 250 255
 Lys Met Ile Glu Tyr His Gly Ser Glu Asn Val Glu Ser Tyr Ile Leu
 260 265 270
 Thr Ile Met Asn Met Val Thr Gly Leu Phe His Asn Pro Ser Ile Gly
 275 280 285
 Asn Ala Ile His Ile Val Val Val Arg Leu Ile Leu Leu Glu Glu Glu
 290 295 300
 Glu Gln Gly Leu Lys Ile Val His His Ala Glu Lys Thr Leu Ser Ser
 305 310 315 320
 Phe Cys Lys Trp Gln Lys Ser Ile Asn Pro Lys Ser Asp Leu Asn Pro
 325 330 335

Val His His Asp Val Ala Val Leu Leu Thr Arg Lys Asp Ile Cys Ala
 340 345 350
 Gly Phe Asn Arg Pro Cys Glu Thr Leu Gly Leu Ser His Leu Ser Gly
 355 360 365
 Met Cys Gln Pro His Arg Ser Cys Asn Ile Asn Glu Asp Ser Gly Leu
 370 375 380
 Pro Leu Ala Phe Thr Ile Ala His Glu Leu Gly His Ser Phe Gly Ile
 385 390 395 400
 Gln His Asp Gly Lys Glu Asn Asp Cys Glu Pro Val Gly Arg His Pro
 405 410 415
 Tyr Ile Met Ser Arg Gln Leu Gln Tyr Asp Pro Thr Pro Leu Thr Trp
 420 425 430
 Ser Lys Cys Ser Glu Glu Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp
 435 440 445
 Gly Phe Cys Leu Asp Asp Ile Pro Lys Lys Lys Gly Leu Lys Ser Lys
 450 455 460
 Val Ile Ala Pro Gly Val Ile Tyr Asp Val His His Gln Cys Gln Leu
 465 470 475 480
 Gln Tyr Gly Pro Asn Ala Thr Phe Cys Gln Glu Val Glu Asn Val Cys
 485 490 495
 Gln Thr Leu Trp Cys Ser Val Lys Gly Phe Cys Arg Ser Lys Leu Asp
 500 505 510
 Ala Ala Ala Asp Gly Thr Gln Cys Gly Glu Lys Lys Trp Cys Met Ala
 515 520 525
 Gly Lys Cys Ile Thr Val Gly Lys Lys Pro Glu Ser Ile Pro Gly Gly
 530 535 540
 Trp Gly Arg Trp Ser Pro Trp Ser His Cys Ser Arg Thr Cys Gly Ala
 545 550 555 560
 Gly Val Gln Ser Ala Glu Arg Leu Cys Asn Asn Pro Glu Pro Lys Phe
 565 570 575
 Gly Gly Lys Tyr Cys Thr Gly Glu Arg Lys Arg Tyr Arg Leu Cys Asn
 580 585 590
 Val His Pro Cys Arg Ser Glu Ala Pro Thr Phe Arg Gln Met Gln Cys
 595 600 605
 Ser Glu Phe Asp Thr Val Pro Tyr Lys Asn Glu Leu Tyr His Trp Phe
 610 615 620
 Pro Ile Phe Asn Pro Ala His Pro Cys Glu Leu Tyr Cys Arg Pro Ile
 625 630 635 640

Asp Gly Gln Phe Ser Glu Lys Met Leu Asp Ala Val Ile Asp Gly Thr
 645 650 655
 Pro Cys Phe Glu Gly Gly Asn Ser Arg Asn Val Cys Ile Asn Gly Ile
 660 665 670
 Cys Lys Met Val Gly Cys Asp Tyr Glu Ile Asp Ser Asn Ala Thr Glu
 675 680 685
 Asp Arg Cys Gly Val Cys Leu Gly Asp Gly Ser Ser Cys Gln Thr Val
 690 695 700
 Arg Lys Met Phe Lys Gln Lys Glu Gly Ser Gly Tyr Val Asp Ile Gly
 705 710 715 720
 Leu Ile Pro Lys Gly Ala Arg Asp Ile Arg Val Met Glu Ile Glu Gly
 725 730 735
 Ala Gly Asn Phe Leu Ala Ile Arg Ser Glu Asp Pro Glu Lys Tyr Tyr
 740 745 750
 Leu Asn Gly Gly Phe Ile Ile Gln Trp Asn Gly Asn Tyr Lys Leu Ala
 755 760 765
 Gly Thr Val Phe Gln Tyr Asp Arg Lys Gly Asp Leu Glu Lys Leu Met
 770 775 780
 Ala Thr Gly Pro Thr Asn Glu Ser Val Trp Ile Gln Leu Leu Phe Gln
 785 790 795 800
 Val Thr Asn Pro Gly Ile Lys Tyr Glu Tyr Thr Ile Gln Lys Asp Gly
 805 810 815
 Leu Asp Asn Asp Val Glu Gln Met Tyr Phe Trp Gln Tyr Gly His Trp
 820 825 830
 Thr Glu Cys Ser Val Thr Cys Gly Thr Gly Ile Arg Arg Gln Thr Ala
 835 840 845
 His Cys Ile Lys Lys Gly Arg Gly Met Val Lys Ala Thr Phe Cys Asp
 850 855 860
 Pro Glu Thr Gln Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys Ala
 865 870 875 880
 Cys Pro Pro Arg Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala Thr
 885 890 895
 Cys Gly Pro His Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln Thr
 900 905 910
 Met Val Ser Asp Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His Leu
 915 920 925
 Leu Lys Pro Lys Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys Pro
 930 935 940

Ser Asp Trp Thr Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys Gly
 945 950 955 960
 Gly Gly Val Arg Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp Glu
 965 970 975
 Pro Cys Asp Val Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly Leu
 980 985 990
 Gln Gln Cys Pro Ser Ser Arg Arg Val Leu Lys Pro Asn Lys Gly Thr
 995 1000 1005
 Ile Ser Asn Gly Lys Asn Pro Pro Thr Leu Lys Pro Val Pro Pro Pro
 1010 1015 1020
 Thr Ser Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met
 1025 1030 1035 1040
 Ser Thr Ser Thr Pro Ala Ile Ser Ser Pro Ser Pro Thr Thr Ala Ser
 1045 1050 1055
 Lys Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln
 1060 1065 1070
 Pro Glu Leu Ser Ser Arg Tyr Leu Ile Ser Thr Gly Ser Thr Ser Gln
 1075 1080 1085
 Pro Ile Leu Thr Ser Gln Ser Leu Ser Ile Gln Pro Ser Glu Glu Asn
 1090 1095 1100
 Val Ser Ser Ser Asp Thr Gly Pro Thr Ser Glu Gly Gly Leu Val Ala
 1105 1110 1115 1120
 Thr Thr Thr Ser Gly Ser Gly Leu Ser Ser Ser Arg Asn Pro Ile Thr
 1125 1130 1135
 Trp Pro Val Thr Pro Phe Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met
 1140 1145 1150
 Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys
 1155 1160 1165
 Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn
 1170 1175 1180
 Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr
 1185 1190 1195 1200
 Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met
 1205 1210 1215
 Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr
 1220 1225 1230
 Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu
 1235 1240 1245

Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn
 1250 1255 1260

Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser
 1265 1270 1275 1280

Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly
 1285 1290 1295

Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly
 1300 1305 1310

Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys
 1315 1320 1325

Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp
 1330 1335 1340

Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His
 1345 1350 1355 1360

Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser
 1365 1370 1375

Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp
 1380 1385 1390

Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala
 1395 1400 1405

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu
 1410 1415 1420

Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly
 1425 1430 1435 1440

Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp
 1445 1450 1455

Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys
 1460 1465 1470

His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly
 1475 1480 1485

Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys
 1490 1495 1500

Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro
 1505 1510 1515 1520

Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu
 1525 1530 1535

Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys
 1540 1545 1550

Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe
 1555 1560 1565

Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln
 1570 1575 1580

Arg Leu Leu Gln Lys Ser Lys Glu Leu
 1585 1590

<210> 31
 <211> 1077
 <212> PRT
 <213> Homo sapiens

<400> 31
 Arg Ser Gln Asp Glu Phe Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala
 1 5 10 15

Phe Pro Thr Arg Val Asp His Asn Gly Ala Leu Leu Ala Phe Ser Pro
 20 25 30

Pro Pro Pro Arg Arg Gln Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser
 35 40 45

Arg Leu Phe Tyr Lys Val Ala Ser Pro Ser Thr His Phe Leu Leu Asn
 50 55 60

Leu Thr Arg Ser Ser Arg Leu Leu Ala Gly His Val Ser Val Glu Tyr
 65 70 75 80

Trp Thr Arg Glu Gly Leu Ala Trp Gln Arg Ala Ala Arg Pro His Cys
 85 90 95

Leu Tyr Ala Gly His Leu Gln Gly Gln Ala Ser Ser Ser His Val Ala
 100 105 110

Ile Ser Thr Cys Gly Gly Leu His Gly Leu Ile Val Ala Asp Glu Glu
 115 120 125

Glu Tyr Leu Ile Glu Pro Leu His Gly Gly Pro Lys Gly Ser Arg Ser
 130 135 140

Pro Glu Glu Ser Gly Pro His Val Val Tyr Lys Arg Ser Ser Leu Arg
 145 150 155 160

His Pro His Leu Asp Thr Ala Cys Gly Val Arg Asp Glu Lys Pro Trp
 165 170 175

Lys Gly Arg Pro Trp Trp Leu Arg Thr Leu Lys Pro Pro Pro Ala Arg
 180 185 190

Pro Leu Gly Asn Glu Thr Glu Arg Gly Gln Pro Gly Leu Lys Arg Ser
 195 200 205

Val Ser Arg Glu Arg Tyr Val Glu Thr Leu Val Val Ala Asp Lys Met

210	215	220
Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu Ala 225 230 235 240		
Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly Ser 245 250 255		
Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp Gln 260 265 270		
Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser Phe 275 280 285		
Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn Ala 290 295 300		
Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile Thr 305 310 315 320		
Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu Gly 325 330 335		
Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser Val 340 345 350		
Asn Glu Asp Ile Gly Leu Pro Gln Ala Phe Thr Ile Ala His Glu Ile 355 360 365		
Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys Gly 370 375 380		
Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr Met 385 390 395 400		
Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Asn Arg Asp Tyr Ile Thr 405 410 415		
Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro Pro 420 425 430		
Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr Asp 435 440 445		
Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln Cys 450 455 460		
Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser Asn 465 470 475 480		
Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys Gln 485 490 495		
Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val Pro 500 505 510		
Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp Thr		

515	520	525
Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser Ser 530 535 540		
Ser Arg His Cys Asp Ser Pro Arg Pro Thr Ile Gly Gly Lys Tyr Cys 545 550 555 560		
Leu Gly Glu Arg Arg Arg His Arg Ser Cys Asn Thr Asp Asp Cys Pro 565 570 575		
Pro Gly Ser Gln Asp Phe Arg Glu Val Gln Cys Ser Glu Phe Asp Ser 580 585 590		
Ile Pro Phe Arg Gly Lys Phe Tyr Lys Trp Lys Thr Tyr Arg Gly Gly 595 600 605		
Gly Val Lys Ala Cys Ser Leu Thr Ser Leu Ala Glu Gly Phe Asn Phe 610 615 620		
Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg Pro 625 630 635 640		
Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly Cys 645 650 655		
Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val Cys 660 665 670		
Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser Pro 675 680 685		
Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys Gly 690 695 700		
Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His Leu 705 710 715 720		
Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro Gly 725 730 735		
Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln Leu 740 745 750		
Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro Ile 755 760 765		
Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro Ala 770 775 780		
Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro Pro 785 790 795 800		
Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys Ala 805 810 815		
Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp Ser		

820					825					830						
Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	Lys	
835					840					845						
Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	Val	
850					855					860						
Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	Ser	
865					870					875					880	
Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	Ala	
885					890					895						
Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	Ala	
900					905					910						
Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	Ser	
915					920					925						
Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	Leu	
930					935					940						
Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	Ser	
945					950					955					960	
Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	Cys	
965					970					975						
Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	Gln	
980					985					990						
Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	Thr	
995					1000					1005						
Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	Thr	
1010					1015					1020						
Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	Pro	
1025					1030					1035					1040	
Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	Leu	
1045					1050					1055						
Lys	Phe	Gln	Phe	Cys	Ser	Arg	Ala	Tyr	Phe	Arg	Gln	Met	Cys	Cys	Lys	
1060					1065					1070						
Thr	Cys	Gln	Gly	His												
1075																

<210> 32

<211> 997

<212> PRT

<213> Homo sapiens

<400> 32

Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro
 1 5 10 15
 Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala
 20 25 30
 Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro
 35 40 45
 Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro
 50 55 60
 Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala
 65 70 75 80
 Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr
 85 90 95
 Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg
 100 105 110
 Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys
 115 120 125
 His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala
 130 135 140
 Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn
 145 150 155 160
 Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly
 165 170 175
 His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu
 180 185 190
 Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val
 195 200 205
 Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln
 210 215 220
 Trp Arg Arg Pro Arg Leu Arg Arg Leu His Gln Arg Ser Val Ser Lys
 225 230 235 240
 Glu Lys Trp Val Glu Thr Leu Val Val Ala Asp Ala Lys Met Val Glu
 245 250 255
 Tyr His Gly Gln Pro Gln Val Glu Ser Tyr Val Leu Thr Ile Met Asn
 260 265 270
 Met Val Ala Gly Leu Phe His Asp Pro Ser Ile Gly Asn Pro Ile His
 275 280 285
 Ile Thr Ile Val Arg Leu Val Leu Leu Glu Asp Glu Glu Glu Asp Leu
 290 295 300

Lys Ile Thr His His Ala Asp Asn Thr Leu Lys Ser Phe Cys Lys Trp
 305 310 315 320
 Gln Lys Ser Ile Asn Met Lys Gly Asp Ala His Pro Leu His His Asp
 325 330 335
 Thr Ala Ile Leu Leu Thr Arg Lys Asp Leu Cys Ala Ala Met Asn Arg
 340 345 350
 Pro Cys Glu Thr Leu Gly Leu Ser His Val Ala Gly Met Cys Gln Pro
 355 360 365
 His Arg Ser Cys Ser Ile Asn Glu Asp Thr Gly Leu Pro Leu Ala Phe
 370 375 380
 Thr Val Ala His Glu Leu Gly His Ser Phe Gly Ile Gln His Asp Gly
 385 390 395 400
 Ser Gly Asn Asp Cys Glu Pro Val Gly Lys Arg Pro Phe Ile Met Ser
 405 410 415
 Pro Gln Leu Leu Tyr Asp Ala Ala Pro Leu Thr Trp Ser Arg Cys Ser
 420 425 430
 Arg Gln Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp Gly Leu Cys Leu
 435 440 445
 Asp Asp Pro Pro Ala Lys Asp Ile Ile Asp Phe Pro Ser Val Pro Pro
 450 455 460
 Gly Val Leu Tyr Asp Val Ser His Gln Cys Arg Leu Gln Tyr Gly Ala
 465 470 475 480
 Tyr Ser Ala Phe Cys Glu Asp Met Asp Asn Val Cys His Thr Leu Trp
 485 490 495
 Cys Ser Val Gly Thr Thr Cys His Ser Lys Leu Asp Ala Ala Val Asp
 500 505 510
 Gly Thr Arg Cys Gly Glu Asn Lys Trp Cys Leu Ser Gly Glu Cys Val
 515 520 525
 Pro Val Gly Phe Arg Pro Glu Ala Val Asp Gly Gly Trp Ser Gly Trp
 530 535 540
 Ser Ala Trp Ser Ile Cys Ser Arg Ser Cys Gly Met Gly Val Gln Ser
 545 550 555 560
 Ala Glu Arg Gln Cys Thr Gln Pro Thr Pro Lys Tyr Lys Gly Arg Tyr
 565 570 575
 Cys Val Gly Glu Arg Lys Arg Phe Arg Leu Cys Asn Leu Gln Ala Cys
 580 585 590
 Pro Ala Gly Arg Pro Ser Phe Arg His Val Gln Cys Ser His Phe Asp
 595 600 605

Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro Val Val Asn
 610 615 620
 Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn Glu Tyr Phe
 625 630 635 640
 Ala Lys Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro Cys Tyr Gln
 645 650 655
 Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys Lys Asn Val
 660 665 670
 Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp Arg Cys Gly
 675 680 685
 Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser Gly Thr Phe
 690 695 700
 Glu Glu Ala Glu Gly Leu Gly Tyr Val Asp Val Gly Leu Ile Pro Ala
 705 710 715 720
 Gly Ala Arg Glu Ile Arg Ile Gln Glu Val Ala Glu Ala Ala Asn Phe
 725 730 735
 Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe Leu Asn Gly Gly
 740 745 750
 Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala Gly Thr Thr Phe
 755 760 765
 Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr Ser Pro Gly Pro
 770 775 780
 Thr Lys Glu Pro Val Trp Ile Gln Val Pro Ala Ser Arg Gly Pro Gly
 785 790 795 800
 Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr Leu His Gly Arg
 805 810 815
 Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr Glu Pro Gly Ser
 820 825 830
 Glu Pro Gly Pro Pro Ala Ala Ala Ser Thr Ser Val Ser Pro Ser Leu
 835 840 845
 Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly Gly Trp Gly Gln
 850 855 860
 Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu Val Leu Met Gly
 865 870 875 880
 Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser Asn Pro Gly Val
 885 890 895
 His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly His Asp Glu Val
 900 905 910

Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp Thr Lys Cys Thr
 915 920 925
 Val Thr Cys Gly Arg Gly Glu Lys Trp Gly Arg His Ser Pro Thr Cys
 930 935 940
 Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His
 945 950 955 960
 Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe
 965 970 975
 Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala
 980 985 990
 Gly Arg Val His Gly
 995

<210> 33
 <211> 854
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu
 1 5 10 15
 Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly
 20 25 30
 Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp
 35 40 45
 Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser
 50 55 60
 Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn
 65 70 75 80
 Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile
 85 90 95
 Thr Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu
 100 105 110
 Gly Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser
 115 120 125
 Val Asn Glu Asp Ile Gly Leu Ala Thr Ala Phe Thr Ile Ala His Glu
 130 135 140
 Ile Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys
 145 150 155 160
 Gly Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr
 165 170 175

Met Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Ser Arg Asp Tyr Ile
 180 185 190
 Thr Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro
 195 200 205
 Pro Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr
 210 215 220
 Asp Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln
 225 230 235 240
 Cys Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser
 245 250 255
 Asn Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys
 260 265 270
 Gln Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val
 275 280 285
 Pro Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp
 290 295 300
 Thr Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser
 305 310 315 320
 Ser Ser Arg His Cys Asp Ser Pro Arg Pro Thr Ile Gly Gly Lys Tyr
 325 330 335
 Cys Leu Gly Glu Arg Arg Arg His Arg Ser Cys Asn Thr Asp Asp Cys
 340 345 350
 Pro Pro Gly Ser Gln Asp Phe Arg Glu Val Gln Cys Ser Glu Phe Asp
 355 360 365
 Ser Ile Pro Phe Arg Gly Lys Phe Tyr Lys Trp Lys Thr Tyr Arg Gly
 370 375 380
 Gly Gly Val Lys Ala Cys Ser Leu Thr Cys Leu Ala Glu Gly Phe Asn
 385 390 395 400
 Phe Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg
 405 410 415
 Pro Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly
 420 425 430
 Cys Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val
 435 440 445
 Cys Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser
 450 455 460
 Pro Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys
 465 470 475 480

Gly Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His
 485 490 495
 Leu Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro
 500 505 510
 Gly Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln
 515 520 525
 Leu Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro
 530 535 540
 Ile Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro
 545 550 555 560
 Ala Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro
 565 570 575
 Pro Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys
 580 585 590
 Ala Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp
 595 600 605
 Ser Ser Ala Val Ala Pro His Tyr Cys Ser Ala His Ser Lys Leu Pro
 610 615 620
 Lys Arg Gln Arg Ala Cys Asn Thr Glu Pro Cys Pro Pro Asp Trp Val
 625 630 635 640
 Val Gly Asn Trp Ser Leu Cys Ser Arg Ser Cys Asp Ala Gly Val Arg
 645 650 655
 Ser Arg Ser Val Val Cys Gln Arg Arg Val Ser Ala Ala Glu Glu Lys
 660 665 670
 Ala Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu
 675 680 685
 Ala Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp
 690 695 700
 Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val
 705 710 715 720
 Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys
 725 730 735
 Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg
 740 745 750
 Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala
 755 760 765
 Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His
 770 775 780

Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr
 785 790 795 800

Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly
 805 810 815

Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val
 820 825 830

Leu Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys
 835 840 845

Lys Thr Cys His Gly His
 850

<210> 34

<211> 860

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (450)

<223> Wherein Xaa is any amino acid.

<400> 34

Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met
 1 5 10 15

Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln
 20 25 30

Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile
 35 40 45

Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp
 50 55 60

Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln
 65 70 75 80

Ala Val Ser Lys Leu Phe Phe Lys Leu Ser Ala Tyr Gly Lys His Phe
 85 90 95

His Leu Asn Leu Thr Leu Asn Thr Asp Phe Val Ser Lys His Phe Thr
 100 105 110

Val Glu Tyr Trp Gly Lys Asp Gly Pro Gln Trp Lys His Asp Phe Leu
 115 120 125

Asp Asn Cys His Tyr Thr Gly Tyr Leu Gln Asp Gln Arg Ser Thr Thr
 130 135 140

Lys Val Ala Leu Ser Asn Cys Val Gly Leu His Gly Val Ile Ala Thr
 145 150 155 160

Glu Asp Glu Glu Tyr Phe Ile Glu Pro Leu Lys Asn Thr Thr Glu Asp
 165 170 175
 Ser Lys His Phe Ser Tyr Glu Asn Gly His Pro His Val Ile Tyr Lys
 180 185 190
 Lys Ser Ala Leu Gln Gln Arg His Leu Tyr Asp His Ser His Cys Gly
 195 200 205
 Val Ser Asp Phe Thr Arg Ser Gly Lys Pro Trp Trp Leu Asn Asp Thr
 210 215 220
 Ser Thr Val Ser Tyr Ser Leu Pro Ile Asn Asn Thr His Ile His His
 225 230 235 240
 Arg Gln Lys Arg Ser Val Ser Ile Glu Arg Phe Val Glu Thr Leu Val
 245 250 255
 Val Ala Asp Lys Met Met Val Gly Tyr His Gly Arg Lys Asp Ile Glu
 260 265 270
 His Tyr Ile Leu Ser Val Met Asn Ile Val Ala Lys Leu Tyr Arg Asp
 275 280 285
 Ser Ser Leu Gly Asn Val Val Asn Ile Ile Val Ala Arg Leu Ile Val
 290 295 300
 Leu Thr Glu Asp Gln Pro Asn Leu Glu Ile Asn His His Ala Asp Lys
 305 310 315 320
 Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser Ile Leu Ser His Gln
 325 330 335
 Ser Asp Gly Asn Thr Ile Pro Glu Asn Gly Ile Ala His His Asp Asn
 340 345 350
 Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Thr Tyr Lys Asn Lys Pro
 355 360 365
 Cys Gly Thr Leu Gly Leu Ala Ser Val Ala Gly Met Cys Glu Pro Glu
 370 375 380
 Arg Ser Cys Ser Ile Asn Glu Asp Ile Gly Leu Gly Ser Ala Phe Thr
 385 390 395 400
 Ile Ala His Glu Ile Val His Asn Phe Gly Met Asn His Asp Gly Ile
 405 410 415
 Gly Asn Ser Cys Gly Arg Lys Val Met Lys Gln Gln Asn Tyr Gly Ser
 420 425 430
 Ser His Tyr Cys Glu Tyr Gln Ser Phe Phe Leu Val Cys Leu Gln Ser
 435 440 445
 Arg Xaa His His Gln Leu Phe Arg Glu Val Cys Arg Glu Leu Trp Cys
 450 455 460

Leu Ser Lys Ser Asn Arg Cys Val Thr Asn Ser Ile Pro Ala Ala Glu
 465 470 475 480
 Gly Thr Leu Cys Gln Thr Gly Asn Ile Glu Lys Gly Trp Cys Tyr Gln
 485 490 495
 Gly Asp Cys Val Pro Phe Gly Thr Trp Pro Gln Ser Ile Asp Gly Gly
 500 505 510
 Trp Gly Pro Trp Ser Leu Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly
 515 520 525
 Gly Val Ser Ser Ser Leu Arg His Cys Asp Ser Pro Ala Pro Ser Gly
 530 535 540
 Gly Gly Lys Tyr Cys Leu Gly Glu Arg Lys Arg Tyr Arg Ser Cys Asn
 545 550 555 560
 Thr Asp Pro Cys Pro Leu Gly Ser Arg Asp Phe Arg Glu Lys Gln Cys
 565 570 575
 Ala Asp Phe Asp Asn Met Pro Phe Arg Gly Lys Tyr Tyr Asn Trp Lys
 580 585 590
 Pro Tyr Thr Gly Gly Gly Val Lys Pro Cys Ala Leu Asn Cys Leu Ala
 595 600 605
 Glu Gly Tyr Asn Phe Tyr Thr Glu Arg Ala Pro Ala Val Ile Asp Gly
 610 615 620
 Thr Gln Cys Asn Ala Asp Ser Leu Asp Ile Cys Ile Asn Gly Glu Cys
 625 630 635 640
 Lys His Val Gly Cys Asp Asn Ile Leu Gly Ser Asp Ala Arg Glu Asp
 645 650 655
 Arg Cys Arg Val Cys Gly Gly Gly Gly Ser Thr Cys Asp Ala Ile Glu
 660 665 670
 Gly Phe Phe Asn Asp Ser Leu Pro Arg Gly Gly Tyr Met Glu Val Val
 675 680 685
 Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met
 690 695 700
 Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile
 705 710 715 720
 Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly
 725 730 735
 Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu
 740 745 750
 Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln
 755 760 765

Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg
 770 775 780
 Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro
 785 790 795 800
 Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg
 805 810 815
 Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr
 820 825 830
 Ala Leu Cys Leu Leu Lys Lys Leu Ile Gly Asn Ile Ser Cys Arg Phe
 835 840 845
 Ala Ser Ser Cys Asn Leu Ala Lys Glu Thr Leu Leu
 850 855 860

<210> 35
 <211> 936
 <212> PRT
 <213> Homo sapiens

<400> 35
 Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
 1 5 10 15
 Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
 20 25 30
 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
 35 40 45
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
 50 55 60
 Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
 65 70 75 80
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
 85 90 95
 Asn Asp Gln Asp Asn Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
 100 105 110
 Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
 115 120 125
 Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
 130 135 140
 Ile Arg Lys Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His
 145 150 155 160
 Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly

				165				170				175			
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180				185						190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
			195				200						205		
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
			210				215						220		
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225				230						235			240		
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
			245						250			255			
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260						265			270			
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
			275									285			
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu
			290			295			300						
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp
305				310						315			320		
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala
			325						330			335			
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val
			340			345						350			
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu
			355			360						365			
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro
			370			375						380			
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn
385				390						395			400		
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile
			405						410			415			
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr
			420						425			430			
Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val
			435			440						445			
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser
			450			455						460			
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr

465		470		475		480
Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg						
	485			490		495
Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala						
	500			505		510
Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala						
	515			520		525
Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser						
	530			535		540
Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu						
	545			550		555
						560
Val Thr Leu Ser Ala Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu						
				570		575
Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser						
	580			585		590
Ala Trp Lys Thr Ala Gln Glu Gly Asp His Gly Ser His Val Tyr Thr						
	595			600		605
Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys						
	610			615		620
Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp						
	625			630		635
						640
Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly						
	645			650		655
His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser						
	660			665		670
Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu						
	675			680		685
Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln						
	690			695		700
Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu						
	705			710		715
						720
His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys						
	725			730		735
Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe						
	740			745		750
Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro						
	755			760		765
Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val						

Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile	100	105	110
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met	115	120	125
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys	130	135	140
Ile	Arg	Lys	Glu	Glu	Pro	His	Thr	Glu	Thr	Val	Arg	Lys	Tyr	Phe	Pro	145	150	155
Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asn	Ser	Ala	Gly	Val	Ala	165	170	175
Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	180	185	190
Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	Gly	Ile	Ser	Ser	Thr	Ala	195	200	205
Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	210	215	220
Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	225	230	235
Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	Gln	Leu	Glu	Ala	Ser	Pro	245	250	255
Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	Gln	Ala	Pro	His	Cys	Ile	260	265	270
Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	Ala	Val	Thr	Pro	Lys	Ser	275	280	285
Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Gln	290	295	300
Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	Pro	Glu	His	Gly	Arg	Lys	305	310	315
Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	Lys	325	330	335
Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Ser	Gly	Gly	Glu	Val	Ser	340	345	350
Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	Val	Val	Glu	Glu	Ser	Ala	355	360	365
Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	370	375	380
Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	385	390	395

Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu
 405 410 415
 Thr Gln Gln Leu Thr Pro Glu Val Lys Ser Lys Ala Ile Gly Tyr Leu
 420 425 430
 Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser
 435 440 445
 Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp
 450 455 460
 Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile
 465 470 475 480
 Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln
 485 490 495
 Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn
 500 505 510
 Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr
 515 520 525
 Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val
 530 535 540
 Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln
 545 550 555 560
 Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr
 565 570 575
 Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys
 580 585 590
 Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu
 595 600 605
 Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln
 610 615 620
 Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr
 625 630 635 640
 Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr
 645 650 655
 Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe
 660 665 670
 Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr
 675 680 685
 Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile
 690 695 700

Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn
 705 710 715 720
 Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr
 725 730 735
 Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu
 740 745 750
 Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly
 755 760 765
 Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser
 770 775 780
 Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser
 785 790 795 800
 Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu
 805 810 815
 Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr
 820 825 830
 Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn
 835 840 845
 Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg
 850 855 860
 Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp
 865 870 875 880
 Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly
 885 890 895

Asn Ala

<210> 37
 <211> 936
 <212> PRT
 <213> Homo sapiens

<400> 37
 Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
 1 5 10 15
 Ser Ala Lys Tyr Asp Val Glu Asn Glu Leu Ala Asn Lys Val Asp Leu
 20 25 30
 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
 35 40 45
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
 50 55 60

Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
 65 70 75 80
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
 85 90 95
 Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
 100 105 110
 Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
 115 120 125
 Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
 130 135 140
 Ile Arg Lys Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His
 145 150 155 160
 Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly
 165 170 175
 Arg Gly His Ala Arg Leu Val His Val Glu Glu Pro His Thr Glu Thr
 180 185 190
 Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val
 195 200 205
 Asn Ser Ala Gly Val Ala Glu Val Gly Val Thr Val Pro Asp Thr Ile
 210 215 220
 Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu
 225 230 235 240
 Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala Phe Gln Pro Phe Phe Val
 245 250 255
 Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu
 260 265 270
 Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys Cys Ile Arg Val Ser Val
 275 280 285
 Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu
 290 295 300
 Gln Ala Pro His Cys Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp
 305 310 315 320
 Ala Val Thr Pro Lys Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala
 325 330 335
 Glu Ala Leu Glu Ser Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val
 340 345 350
 Pro Glu His Gly Arg Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu
 355 360 365

Pro Glu Gly Leu Glu Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro
 370 375 380
 Ser Gly Gly Glu Val Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn
 385 390 395 400
 Val Val Glu Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile
 405 410 415
 Leu Gly Ser Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr
 420 425 430
 Gly Cys Gly Glu Glx Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val
 435 440 445
 Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser
 450 455 460
 Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr
 465 470 475 480
 Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg
 485 490 495
 Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala
 500 505 510
 Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala
 515 520 525
 Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser
 530 535 540
 Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu
 545 550 555 560
 Val Thr Leu Ser Ala Tyr Ile Lys Ile Ala Leu Leu Glu Ile Pro Leu
 565 570 575
 Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser
 580 585 590
 Ala Trp Lys Thr Ala Glu Glu Gly Asp His Gly Ser His Val Tyr Thr
 595 600 605
 Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys
 610 615 620
 Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp
 625 630 635 640
 Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly
 645 650 655
 His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser
 660 665 670

Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu
 675 680 685
 Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln
 690 695 700
 Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Lys Val Val Ala Leu
 705 710 715 720
 His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys
 725 730 735
 Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe
 740 745 750
 Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro
 755 760 765
 Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val
 770 775 780
 Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu
 785 790 795 800
 Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu
 805 810 815
 Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr
 820 825 830
 Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val
 835 840 845
 Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser
 850 855 860
 Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr
 865 870 875 880
 Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu
 885 890 895
 Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr
 900 905 910
 Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro
 915 920 925
 Cys Ser Lys Asp Leu Gly Asn Ala
 930 935

<210> 38
 <211> 931
 <212> PRT
 <213> Rattus norvegicus

<400> 38

Arg Leu Val Leu Tyr Ala Ile Leu Pro Asn Gly Glu Val Val Gly Asp
1 5 10 15

Thr Ala Lys Tyr Glu Ile Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
20 25 30

Val Phe Arg Pro Asn Ser Gly Leu Pro Ala Thr Arg Ala Leu Leu Ser
35 40 45

Val Met Ala Ser Pro Gln Ser Leu Cys Gly Leu Arg Ala Val Asp Gln
50 55 60

Ser Val Leu Leu Met Lys Pro Glu Thr Glu Leu Ser Ala Ser Leu Ile
65 70 75 80

Tyr Asp Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gln Gly Ala
85 90 95

Asp Gln Arg Glu Glu Asp Thr Asn Gly Cys Val Lys Gln Asn Asp Thr
100 105 110

Tyr Ile Asn Gly Ile Leu Tyr Ser Pro Val Gln Asn Thr Asn Glu Glu
115 120 125

Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn
130 135 140

Ser Asn Ile Arg Lys Pro Lys Val Cys Glu Arg Leu Arg Asp Asn Lys
145 150 155 160

Gly Ile Pro Ala Ala Tyr His Leu Val Ser Gln Ser His Met Asp Ala
165 170 175

Phe Leu Glu Ser Ser Glu Ser Pro Thr Glu Thr Arg Arg Ser Tyr Phe
180 185 190

Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asp Ser Ala Gly Val
195 200 205

Ala Glu Val Glu Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala
210 215 220

Gly Ala Phe Cys Leu Ser Asn Asp Thr Gly Leu Gly Leu Ser Pro Val
225 230 235 240

Val Gln Phe Gln Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro
245 250 255

Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu
260 265 270

Asn Tyr Leu Pro Thr Cys Ile Arg Val Ala Val Gln Leu Glu Ala Ser
275 280 285

Pro Asp Phe Leu Ala Ala Pro Glu Glu Lys Glu Gln Arg Ser His Cys

290	295	300
Ile Cys Met Asn Gln Arg His Thr Ala Ser Trp Ala Val Ile Pro Lys 305 310 315 320		
Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Asn Ser 325 330 335		
Lys Glu Leu Cys Gly Asn Glu Val Pro Val Val Pro Glu Gln Gly Lys 340 345 350		
Lys Asp Thr Ile Ile Lys Ser Leu Leu Val Glu Pro Glu Gly Leu Glu 355 360 365		
Asn Glu Val Thr Phe Asn Ser Leu Leu Cys Pro Met Gly Ala Glu Val 370 375 380		
Ser Glu Leu Ile Ala Leu Lys Leu Pro Ser Asp Val Val Glu Glu Ser 385 390 395 400		
Ala Arg Ala Ser Val Thr Val Leu Gly Asp Ile Leu Gly Ser Ala Met 405 410 415		
Gln Asn Thr Gln Asp Leu Leu Lys Met Pro Tyr Gly Cys Gly Glu Gln 420 425 430		
Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn 435 440 445		
Glu Thr Gln Gln Leu Thr Gln Glu Ile Lys Thr Lys Ala Ile Ala Tyr 450 455 460		
Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Arg Asp Gly 465 470 475 480		
Ser Tyr Ser Ala Phe Gly Asp Lys Pro Gly Arg Asn His Ala Asn Thr 485 490 495		
Trp Leu Thr Ala Phe Val Leu Lys Ser Phe Ala Gln Ala Arg Lys Tyr 500 505 510		
Ile Phe Ile Asp Glu Val His Ile Thr Gln Ala Leu Leu Trp Leu Ser 515 520 525		
Gln Gln Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu 530 535 540		
Asn Asn Ala Met Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala 545 550 555 560		
Tyr Ile Thr Ile Ala Leu Leu Glu Met Ser Leu Pro Val Thr His Pro 565 570 575		
Val Val Arg Asn Ala Leu Phe Cys Leu Asp Thr Ala Trp Lys Ser Ala 580 585 590		
Arg Gly Gly Ala Gly Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala		

595					600					605					
Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys
610						615					620				
Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	Arg	Gly	Gly	Ala	Gly	Gly	Ser	His
625					630					635					640
Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro
				645					650					655	
Gln	Ala	Thr	Ser	Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Val	Leu	Leu	Ala
			660					665					670		
Tyr	Leu	Thr	Thr	Glu	Pro	Ala	Pro	Thr	Gln	Glu	Asp	Leu	Thr	Ala	Ala
			675				680					685			
Met	Leu	Ile	Val	Lys	Trp	Leu	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly
690					695						700				
Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys
705				710					715						720
Tyr	Gly	Ser	Ala	Thr	Phe	Thr	Arg	Ala	Lys	Lys	Ala	Ala	Gln	Val	Thr
				725					730					735	
Ile	Arg	Ser	Ser	Gly	Thr	Phe	Ser	Thr	Lys	Phe	Gln	Val	Asn	Asn	Asn
				740				745					750		
Asn	Gln	Leu	Leu	Leu	Gln	Arg	Val	Thr	Leu	Pro	Thr	Val	Pro	Gly	Asp
				755			760					765			
Tyr	Thr	Val	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser
				770		775					780				
Leu	Lys	Tyr	Ser	Val	Leu	Pro	Arg	Glu	Glu	Glu	Phe	Pro	Phe	Ala	Val
785				790					795						800
Val	Val	Gln	Thr	Leu	Pro	Gly	Thr	Cys	Glu	Asp	Pro	Lys	Ala	His	Thr
				805					810					815	
Ser	Phe	Gln	Ile	Ser	Leu	Asn	Ile	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Glu
				820				825					830		
Ser	Asn	Met	Ala	Ile	Ala	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro
				835			840					845			
Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Val	His	Val	Ser	Arg
				850		855					860				
Thr	Glu	Val	Ser	Asn	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser
865				870					875					880	
Asn	Gln	Thr	Val	Asn	Leu	Ser	Phe	Thr	Val	Gln	Gln	Asp	Ile	Pro	Ile
				885					890					895	
Arg	Asp	Leu	Lys	Pro	Ala	Val	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Lys

900	905	910
Asp Glu Phe Ala Val Ala Lys Tyr Ser Ala Pro Cys Ser Thr Asp Tyr		
915	920	925
Gly Asn Ala		
930		
<210> 39		
<211> 941		
<212> PRT		
<213> Cavia porcellus		
<400> 39		
Arg Val Leu Ile Tyr Ala Ile Leu Pro Ser Gly Glu Ile Ile Ala Asp		
1	5	10 15
Ser Ala Lys Tyr Asn Val Glu Asn Cys Leu Asp Asn Lys Val Asn Leu		
20	25	30
Ser Phe Ser Glu Gly Gln Ser Leu Pro Ala Ser Lys Thr His Leu Arg		
35	40	45
Val Thr Ala Ser Pro Gln Ser Leu Cys Ala Leu Arg Ala Val Asp Gln		
50	55	60
Ser Val Leu Leu Arg Lys Pro Glu Ala Val Leu Ser Ala Ser Ser Val		
65	70	75 80
Tyr Ala Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gly Leu Leu		
85	90	95
Gly Gln Gln Glu Glu Asn Asp Gly Glu Cys Val Ser Leu Tyr Asn Thr		
100	105	110
Tyr Ile Asp Gly Ile Leu Tyr Ser Pro Glu Pro Asn Ile Asn Glu Lys		
115	120	125
Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn		
130	135	140
Thr Lys Ile Gln Lys Pro Gln Leu Cys Ala His Val Gln Lys Phe Glu		
145	150	155 160
Val Pro Thr Met Ala Tyr Ser Tyr Ser Glu Ser Ser Ser Phe Arg Ser		
165	170	175
Gly Pro Arg Arg Val Pro Ala Val Gly Ile Ala Ala Thr Tyr Ser Glu		
180	185	190
Pro Pro Lys Glu Thr Val Arg Thr Tyr Ser Pro Glu Thr Trp Ile Trp		
195	200	205
Asp Leu Lys Val Thr Asp Ser Ser Gly Val Ala Glu Val Glu Val Thr		
210	215	220

Val 225	Pro	Asp	Thr	Ile	Thr 230	Glu	Trp	Lys	Ala	Gly 235	Ala	Phe	Cys	Leu	Ser 240
Asn	Asp	Thr	Gly	Leu 245	Gly	Leu	Ser	Pro	Thr 250	Ala	Ser	Leu	Arg	Ala 255	Phe
Gln	Pro	Phe	Phe 260	Val	Glu	Leu	Thr	Met 265	Pro	Tyr	Ser	Val	Ile 270	Arg	Gly
Glu	Ala	Phe 275	Thr	Leu	Lys	Ala	Thr 280	Val	Leu	Asn	Tyr	Leu 285	Pro	Asp	Cys
Ile 290	Arg	Ile	Ser	Val	His 295	Leu	Glu	Ala	Ser	Pro 300	Lys	Phe	Leu	Ala	Glu
Pro 305	Lys	Ala	Lys	Glu	Gln 310	Glu	Ser	Tyr	Cys	Val 315	Cys	Gly	Asn	Glu	Arg 320
Gln	Thr	Val	Ser 325	Trp	Val	Val	Thr	Pro	Lys 330	Ser	Leu	Gly	Asn 335	Val	Asn
Phe	Thr	Val 340	Ser	Ala	Glu	Ala	Leu	Glu 345	Ser	Ser	Glu	Leu	Cys 350	Gly	Asn
Glu	Lys 355	Thr	Val	Val	Pro	Thr	Tyr 360	Gly	Lys	Lys	Asp	Thr 365	Ile	Ile	Lys
Pro 370	Leu	Leu	Val	Glu	Pro	Glu	Gly 375	Ile	Glu	Lys 380	Glu	Glu	Thr	Trp	Thr
Ser 385	Leu	Ile	Arg	Val	Ser 390	Asp	Thr	Thr	Val	Ser 395	Glu	Lys	Leu	His	Leu 400
Glu	Leu	Pro	Ser 405	Asn	Val	Ile	Gln	Asp	Ser 410	Ala	Arg	Ala	Thr	Val 415	Ser
Ile	Leu	Gly	Asp 420	Ile	Leu	Gly	Ser	Ala 425	Met	Gln	Asn	Ile	Gln 430	Asn	Leu
Leu	Gln 435	Met	Pro	Tyr	Gly	Cys	Gly 440	Glu	Gln	Asn	Met 445	Val	Leu	Phe	Ala
Pro 450	Asn	Ile	Tyr	Val	Leu	Asp 455	Tyr	Leu	Asn	Glu	Thr 460	Gln	Gln	Leu	Thr
Pro 465	Asp	Ile	Lys	Ser	Lys 470	Ala	Ile	Ser	Tyr	Leu 475	Ser	Thr	Gly	Tyr	Gln 480
Arg	Gln	Leu	Asn 485	Tyr	Lys	His	Arg	Asp	Gly 490	Ser	Tyr	Ser	Thr	Phe 495	Gly
Glu	Asn	Tyr	Arg 500	Gly	Gly	Gln	Gly	Asn 505	Thr	Trp	Leu	Thr	Ala 510	Phe	Val
Leu	Lys 515	Thr	Phe	Ser	Gln	Ala	Arg 520	Lys	Tyr	Ile	Phe 525	Ile	Asp	Glu	Ala

His Ile Thr Gln Ala Leu Ser Trp Leu Ser Gln Lys Gln Lys Asp Asn
 530 535 540
 Gly Cys Phe Trp Ser Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly
 545 550 555 560
 Gly Val Glu Asp Glu Ile Ser Leu Ser Ala Tyr Ile Thr Ile Ala Leu
 565 570 575
 Leu Glu Met Ser Leu Pro Asp Thr His Pro Val Val Arg Asn Ala Leu
 580 585 590
 Phe Cys Leu Glu Ser Ala Trp Lys Ser Ala Lys Glu Gly Thr His Gly
 595 600 605
 Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala
 610 615 620
 Gly Asn Gln Glu Arg Lys Lys Glu Ile Leu Lys Ser Leu Glu Asp Glu
 625 630 635 640
 Gly Val Lys Glu Asp Asn Ser Leu His Trp Ala Arg Pro Gln Lys Pro
 645 650 655
 Lys Val Ser Glu Gly Phe Leu Phe Lys Ser Gln Ala Pro Ser Ala Glu
 660 665 670
 Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr Leu Thr Ala Arg Pro
 675 680 685
 Ala Pro Thr Pro Glu Asp Leu Thr Ser Ala Thr Asp Ile Val Asn Trp
 690 695 700
 Val Thr Lys Gln Gln Asn Ser His Gly Gly Tyr Ser Ser Thr Gln Asp
 705 710 715 720
 Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr Ala Ala Ala Thr Phe
 725 730 735
 Thr Arg Thr Glu Lys Ala Ala Gln Val Thr Ile Lys Ser Ser Gly Thr
 740 745 750
 Phe Ser Thr Asn Phe Glu Val Asn His Asn Asn Arg Leu Leu Leu Gln
 755 760 765
 Gln Val Ser Leu Pro Thr Val Ser Asp Ser Tyr Thr Ile Thr Val Thr
 770 775 780
 Gly Glu Gly Asn Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Val Pro
 785 790 795 800
 Ser Glu Lys Gly Thr Phe Pro Phe Ala Leu Glu Ala Glu Thr Val Pro
 805 810 815
 Gln Ala Cys Asp Gly Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu
 820 825 830

Asn Val Ser Tyr Ile Gly Ser Arg Pro Val Ser Asn Met Ala Ile Val
835 840 845

Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys
850 855 860

Asn Leu Glu Lys Ser Glu His Ile Ser Arg Thr Glu Val Ser Asn Asn
865 870 875 880

His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu
885 890 895

Ser Phe Phe Val Val Gln Asp Ile Glu Val Arg Asp Leu Lys Pro Ala
900 905 910

Ile Ile Lys Val Tyr Asp Tyr Tyr Glu Thr Asn Glu Phe Ala Ile Ala
915 920 925

Glu Tyr His Ala Pro Cys Ser Lys Asp Pro Gly Asn Ala
930 935 940

<210> 40

<211> 373

<212> PRT

<213> Mus musculus

<400> 40

Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr
1 5 10 15

Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu
20 25 30

Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser
35 40 45

Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg
50 55 60

Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro
65 70 75 80

Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln
85 90 95

Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser
100 105 110

Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
115 120 125

Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
130 135 140

Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile
145 150 155 160

Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val
165 170 175

Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val
180 185 190

Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val
195 200 205

Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr
210 215 220

Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly
225 230 235 240

Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr
245 250 255

Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met
260 265 270

Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe
275 280 285

Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val
290 295 300

Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg
305 310 315 320

Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu
325 330 335

Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly
340 345 350

Pro Val Gln Pro Glu Gln His His Arg Ala Ala Glu Leu Thr Ser His
355 360 365

Ile Pro Ser Cys Glu
370

<210> 41

<211> 347

<212> PRT

<213> *Oryzctolagus cuniculus*

<400> 41

Met Ser Asn Leu Thr Val Gly Cys Leu Ala Asn Ala Thr Val Cys Glu
1 5 10 15

Gly Ala Ser Cys Val Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser
20 25 30

Val Val Leu Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe

35	40	45
Ser Met Gly Cys Asn Val Glu Ile Lys Lys Phe Leu Gly His Ile Arg		
50	55	60
Arg Pro Trp Gly Ile Phe Ile Gly Phe Leu Cys Gln Phe Gly Ile Met		
65	70	75
Pro Leu Thr Gly Phe Val Leu Ala Val Ala Phe Gly Ile Met Pro Ile		
	85	90
Gln Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Ala		
	100	105
Ser Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val		
	115	120
Ser Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu		
	130	135
Cys Leu Tyr Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val		
145	150	155
Ile Pro Tyr Asp Asn Ile Gly Thr Ser Leu Val Ala Leu Val Val Pro		
	165	170
Val Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys		
	180	185
Ile Ile Leu Lys Val Gly Ser Ile Ala Gly Ala Val Leu Ile Val Leu		
	195	200
Ile Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu		
	210	215
Pro Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Met Ala Gly Tyr Ser		
225	230	235
Leu Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys		
	245	250
Arg Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser		
	260	265
Thr Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Thr Tyr Val Phe		
	275	280
Thr Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile		
	290	295
Phe Leu Gly Ile Tyr Val Ala Tyr Arg Lys Cys His Gly Lys Asn Asp		
305	310	315
Ala Glu Phe Pro Asp Ile Lys Asp Thr Lys Thr Glu Pro Glu Ser Ser		
	325	330
Phe His Gln Met Asn Gly Gly Phe Gln Pro Glu		

340

345

<210> 42

<211> 348

<212> PRT

<213> Rattus norvegicus

<400> 42

Met Asp Asn Ser Ser Val Cys Ser Pro Asn Ala Thr Phe Cys Glu Gly
 1 5 10 15

Asp Ser Cys Leu Val Thr Glu Ser Asn Phe Asn Ala Ile Leu Ser Thr
 20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
 35 40 45

Met Gly Cys Asn Val Glu Ile Asn Lys Phe Leu Gly His Ile Lys Arg
 50 55 60

Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80

Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
 85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
 100 105 110

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
 115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
 130 135 140

Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
 145 150 155 160

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
 165 170 175

Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190

Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
 195 200 205

Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
 210 215 220

Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
 225 230 235 240

Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255

Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
260 265 270

Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
275 280 285

Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Ile Ile
290 295 300

Leu Gly Met Tyr Val Thr Tyr Lys Lys Cys His Gly Lys Asn Asp Ala
305 310 315 320

Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe
325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
340 345

<210> 43

<211> 348

<212> PRT

<213> Mus musculus

<400> 43

Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
1 5 10 15

Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45

Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg
50 55 60

Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80

Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140

Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175

Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190
 Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile
 195 200 205
 Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
 210 215 220
 Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile
 290 295 300
 Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala
 305 310 315 320
 Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe
 325 330 335
 Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 44
 <211> 348
 <212> PRT
 <213> Mus musculus

<400> 44
 Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
 1 5 10 15
 Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
 20 25 30
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
 35 40 45
 Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg
 50 55 60
 Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80
 Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln

Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly
 1 5 10 15
 Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val
 20 25 30
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser
 35 40 45
 Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg
 50 55 60
 Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80
 Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln
 85 90 95
 Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser
 100 105 110
 Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser
 115 120 125
 Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
 130 135 140
 Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
 145 150 155 160
 Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val
 165 170 175
 Ser Ile Gly Met Tyr Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190
 Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
 195 200 205
 Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Thr Ile Glu Pro
 210 215 220
 Lys Leu Trp Ile Ile Gly Thr Ile Tyr Pro Ile Ala Gly Tyr Gly Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Leu Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile Leu
 290 295 300

Leu Gly Ala Tyr Val Ala Tyr Lys Lys Cys His Gly Lys Asn Asn Thr
 305 310 315 320

Glu Leu Gln Glu Lys Thr Asp Asn Glu Met Glu Pro Arg Ser Ser Phe
 325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15

Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30

Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45

Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60

Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80

Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95

Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr Ser Ile Gly Glu
 100 105 110

Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125

Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140

Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160

Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175

Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190

Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
 195 200 205

Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
 210 215 220

Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys
 225 230 235 240
 Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn
 245 250 255
 Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln
 260 265 270

<210> 47
 <211> 272
 <212> PRT
 <213> Rattus norvegicus

<400> 47
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu
 100 105 110
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140
 Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160
 Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175
 Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190
 Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys

195	200	205
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile		
210	215	220
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys		
225	230	235
Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn		
	245	250
Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln		
	260	270

<210> 48
 <211> 1798
 <212> PRT
 <213> Drosophila melanogaster

<400> 48
 Met Glu Met Arg Glu Val Leu Ser Arg Glu Gly Arg Glu Ala Lys Asn
 1 5 10 15
 Leu Leu Val Tyr Gln Phe Cys Asp Glu Thr Thr Ser Ser Gly Ala Thr
 20 25 30
 Ser Gly Phe Gly Ser Thr Gly Gly Asp Val Gly Gly Gly Ser Gly Gly
 35 40 45
 Asp Gly Pro Ala Val Gly Ser Gly Gly Val Leu Leu Asn Gly Asp Cys
 50 55 60
 Tyr Arg Lys Pro Pro Met Val Pro Pro Lys Ser Pro Asn Gly Thr Pro
 65 70 75 80
 Lys Asn Cys Gln Ser Pro Thr Ser Pro Arg Leu Lys Ser Ser Ala Ser
 85 90 95
 Val Gly Cys Gly Gly Gly Ser Ser Gly Gly Pro Arg Val Arg Ser Ala
 100 105 110
 Ser Thr Gly Arg Asp Lys Lys Ser Glu Leu Gln Ala Arg Tyr Trp Ala
 115 120 125
 Leu Leu Phe Gly Asn Leu Gln Arg Ala Ile Asn Glu Ile Tyr Gln Thr
 130 135 140
 Val Glu Cys Tyr Glu Asn Ile Ser Ser Cys Gln Glu Thr Ile Leu Val
 145 150 155 160
 Leu Glu Asn Tyr Val Arg Asp Phe Lys Ala Leu Cys Glu Trp Phe Lys
 165 170 175

Val	Ser	Trp	Asp	Tyr	Glu	Ser	Arg	Pro	Leu	Gln	Gln	Arg	Pro	Gln	Ser	180	185	190	
Leu	Ala	Trp	Glu	Val	Arg	Lys	Ser	Asn	Pro	Thr	Pro	Arg	Val	Arg	Thr	195	200	205	
Arg	Ser	Leu	Cys	Ser	Pro	Asn	Asn	Ser	Gly	Lys	Ser	Ser	Pro	Ala	Leu	210	215	220	
Phe	Pro	Gly	Thr	Gln	Ser	Gly	Glu	Thr	Ser	Pro	Phe	Cys	Asp	Asn	Gly	225	230	235	240
Gln	Ile	Ser	Pro	Arg	Lys	Leu	Leu	Arg	Ala	Tyr	Asp	Gln	Val	Pro	Lys	245	250	255	
Gly	Ala	Met	Arg	Leu	Asn	Val	Arg	Glu	Leu	Phe	Ala	Ala	Ser	Lys	Arg	260	265	270	
Ala	Thr	Gln	Gly	Ser	Ser	Gln	Ser	Asp	Asn	Met	Glu	Gly	Pro	Leu	Asp	275	280	285	
Leu	Ser	Gly	Asp	Lys	Ser	Asn	Phe	Val	Leu	Arg	Ser	Thr	Gln	Tyr	Ala	290	295	300	
Gln	Thr	Asp	Leu	Glu	Asp	Pro	His	Leu	Thr	Leu	Ala	Asp	Val	Arg	Glu	305	310	315	320
Lys	Met	Arg	Met	Glu	Ala	Glu	Glu	Arg	Glu	Ala	Gln	Asn	Arg	Ile	Glu	325	330	335	
Asn	Glu	Ala	Leu	Glu	Glu	Val	Thr	Ile	Pro	Ile	Asp	Asn	Glu	Asp	Ala	340	345	350	
Thr	Glu	Ser	Leu	Asn	Lys	Gln	Glu	Pro	Ser	Ser	Leu	Glu	Leu	Pro	Ile	355	360	365	
His	Asn	Val	Ala	Asp	Leu	Ser	Lys	Glu	Pro	Glu	Leu	Met	Glu	Ala	Ala	370	375	380	
Ser	Glu	Ala	Thr	Ala	Leu	Glu	Met	Thr	Val	Ala	Ser	Leu	Glu	Ser	Met	385	390	395	400
Glu	Asn	Ala	Leu	Leu	Asn	Gln	Gln	Ala	Asn	Lys	Glu	Pro	Thr	Pro	Pro	405	410	415	
Ser	Thr	Val	Ile	Lys	Pro	Leu	Ala	Glu	Ile	Leu	Lys	Lys	Pro	Gln	Pro	420	425	430	
Leu	Asn	Pro	Leu	Ser	Gly	Asn	Asn	Val	Gln	Asn	Ser	Pro	Leu	Lys	Tyr	435	440	445	
Ser	Ser	Val	Leu	Asn	Arg	Pro	Ser	Lys	Lys	Met	Ile	Pro	Pro	Pro	Gly	450	455	460	
Gly	Val	Ala	Ala	Gln	Lys	Thr	Ile	Ser	Thr	Lys	Pro	Gly	Leu	Val	Lys	465	470	475	480

Pro Asn Leu Thr Thr Thr Val Asn Gly Leu Arg Ser Thr Lys Thr Ala
 485 490 495
 Thr Ala Pro Pro Ala Ile Lys Thr Thr Gly Arg Ser Gly Leu Gln Arg
 500 505 510
 His Pro Arg Pro Ser Ser Lys Thr Glu Cys Tyr Gly Pro Pro Asn Asn
 515 520 525
 Val Ala Ser Arg Leu Ser Ala Arg Ser Arg Thr Ile Asn Thr Leu Lys
 530 535 540
 Ala Glu Asn Gln His Ser Glu Pro Lys Gln Ile Gln Pro Pro Thr Asp
 545 550 555 560
 Ala Asp Asp Gly Trp Leu Thr Val Lys Asn Arg Arg Arg Thr Ser Met
 565 570 575
 His Trp Ala Asn Arg Phe Asn Gln Pro Thr Gly Tyr Ala Ser Leu Pro
 580 585 590
 Thr Leu Ala Leu Leu Asn Glu Gln Gln Lys Glu Gln Glu His Lys Glu
 595 600 605
 Lys Gln Lys Gly Glu Asp Asp Gly Lys Val Ile Val Lys Thr Ile Ser
 610 615 620
 Ala Lys Thr Lys Ala Pro Ile Glu Val Ala Lys Ala Lys Ala Lys Thr
 625 630 635 640
 Ser Ile Val Ile Thr Arg Pro Glu Ile Lys Asn Ala Lys Ala Lys Val
 645 650 655
 Asn Ser Phe Pro Val Gln Lys Ser Asn Thr Asn Gln Val Lys Lys Pro
 660 665 670
 Glu Lys Gln Glu Lys Ser Asp Thr Thr Ala Pro Ala Ala Ile Ala Ser
 675 680 685
 Ser Arg Leu Lys Met Thr Ser Leu His Lys Glu Tyr Met Arg Ser Glu
 690 695 700
 Lys Asn Ala Leu Arg Lys Leu Gln Gln Lys Glu Gln Gly Asn Gln Gln
 705 710 715 720
 His Asn Ser Ser Ser Ser Ser Ala Glu Thr Val Val Glu Ser Cys Asn
 725 730 735
 Glu Asp His Ser Lys Ile Asp Ile Lys Ile Gln Thr Asn Cys Glu Phe
 740 745 750
 Ser Lys Thr Ile Gly Glu Leu Tyr Glu Ser Ile Ala His Cys Lys Leu
 755 760 765
 Pro Ser Gly Ser Leu Lys Thr Asn Ala Ser Thr Leu Ser Ala Cys Asp
 770 775 780

Glu	Asn	Glu	Glu	Gln	Asn	Thr	Asp	Asp	Asn	Glu	Glu	Glu	Arg	Asn	Glu		785		790		795		800
Arg	Ile	Leu	Gly	Glu	Val	Gln	Glu	Ser	Leu	Glu	Arg	Gln	Ile	Arg	Glu			805		810		815	
Leu	Glu	Gln	Thr	Glu	Ile	Asp	Val	Asp	Thr	Glu	Thr	Asp	Glu	Thr	Asp			820		825		830	
Cys	Glu	Val	Gln	Leu	Glu	Glu	Gln	Asp	Asp	Gly	Val	Asp	Gly	Leu	Glu			835		840		845	
Met	Gly	Ser	Gly	Asp	Asp	Ser	Ala	Val	Phe	Val	Thr	Met	Ser	Asp	Asp		850		855		860		
Glu	Asn	Ala	Ser	Leu	Glu	Leu	Arg	Tyr	Gln	Ala	Leu	Leu	Ser	Asp	Met		865		870		875		880
Ser	Trp	Asn	Glu	Arg	Ala	Glu	Ala	Leu	Ala	Thr	Leu	Gln	Ala	Tyr	Val			885		890		895	
Ala	Arg	His	Pro	Gly	Arg	Ala	Gln	Glu	Leu	His	Gln	Lys	Leu	Ser	Ser			900		905		910	
Pro	Ser	Arg	Arg	Arg	Ser	Leu	Gln	Glu	Thr	Leu	Lys	Lys	Tyr	Gln	Ala			915		920		925	
Lys	Gln	Ala	Arg	Ala	Gln	Gln	Lys	Arg	Asn	Leu	Leu	Gln	Gln	Glu	Lys		930		935		940		
Ala	Ala	Lys	Leu	Gln	Gln	Leu	Phe	Ser	Arg	Val	Glu	Asp	Val	Lys	Ala		945		950		955		960
Ala	Lys	Asn	Gln	Ile	Ile	Glu	Asp	Lys	Arg	Gln	Lys	Met	Gln	Gly	Arg			965		970		975	
Leu	Gln	Arg	Ala	Ala	Glu	Asn	Arg	Glu	Gln	Tyr	Leu	Lys	Gln	Ile	Ile			980		985		990	
Glu	Lys	Ala	His	Asp	Glu	Glu	Lys	Lys	Leu	Lys	Glu	Ile	Asn	Phe	Ile		995		1000		1005		
Lys	Asn	Ile	Glu	Ala	Gln	Asn	Lys	Arg	Leu	Asp	Leu	Leu	Glu	Ser	Ser		1010		1015		1020		
Lys	Glu	Thr	Glu	Gly	Arg	Leu	Gln	Asp	Leu	Glu	Gln	Glu	Arg	Gln	Lys		1025		1030		1035		1040
Arg	Val	Glu	Glu	Lys	Leu	Ala	Lys	Glu	Ala	Ala	Val	Glu	Arg	Arg	Arg			1045		1050		1055	
Gln	Ala	Leu	Glu	Lys	Glu	Arg	Leu	Leu	Lys	Leu	Glu	Lys	Met	Asn	Glu			1060		1065		1070	
Thr	Arg	Leu	Glu	Lys	Glu	Gln	Arg	Ile	Gly	Lys	Met	Gln	Glu	Gln	Lys		1075		1080		1085		

Glu Lys Gln Arg Gln Ala Leu Ala Arg Glu Lys Ala Arg Asp Arg Glu
 1090 1095 1100
 Glu Arg Leu Leu Ala Leu Gln Val Gln Gln Gln Gln Thr Thr Glu Glu
 1105 1110 1115 1120
 Leu Gln Arg Lys Ile Leu Gln Lys Gln Met Glu Ser Ala Arg Arg His
 1125 1130 1135
 Glu Glu Asn Ile Glu His Ile Arg Gln Arg Ala Leu Glu Leu Thr Ile
 1140 1145 1150
 Pro Thr Arg Gln Ala Asp Glu Gly Arg Gly Asp Gln Asp Val Ser Glu
 1155 1160 1165
 Asp Ile Leu Asn Gly Asn Ala Thr Ser Thr Thr Asn Glu Asp Cys Asp
 1170 1175 1180
 Leu Ser Ser Ser Leu Ser Glu Val Gly Gly Asn Asn Ala His Thr Arg
 1185 1190 1195 1200
 Ser Tyr Lys Lys Lys Met Lys Lys Leu Lys Gln Arg Met Asn Gln Cys
 1205 1210 1215
 Ala Ala Glu Tyr Leu Glu Ser Leu Glu Ala Leu Pro Ala His Ala Arg
 1220 1225 1230
 Arg Asp Ser Thr Val Pro Lys Leu Leu Asn Leu Val Val Lys Gly Gly
 1235 1240 1245
 Gly Ala Gln Gly Leu Asp Arg Asn Leu Gly Asn Leu Leu Arg Val Ile
 1250 1255 1260
 Pro Lys Ala Gln Thr Leu Asp Phe Leu Ala Phe Leu Cys Met Asp Gly
 1265 1270 1275 1280
 Leu Gly Ile Leu Ala Asn His Val Ile Ser Lys Gly Met Asp Glu Asn
 1285 1290 1295
 Ser Glu Ile Ser Arg Lys Ser Val Tyr Leu Ala Ala Gln Leu Tyr Arg
 1300 1305 1310
 Asn Ala Cys Ser Val Cys Pro Gln Ile Ala Arg His Ala Leu Leu Gly
 1315 1320 1325
 Asn Ser Ile Thr Val Leu Phe Asp Ala Ile Asn Lys Ser Phe Gln Val
 1330 1335 1340
 Ile Leu Lys Ser Asn Arg Cys Thr Lys Glu Thr Phe Ser Asn Phe Trp
 1345 1350 1355 1360
 Pro Pro Lys Met Leu His Asn Lys Ser Val Ala Arg Gln Ser Ser Arg
 1365 1370 1375
 Leu Glu Ala Leu Ser Leu Pro Glu Glu Lys Ser Pro Gln His Pro Val
 1380 1385 1390

Glu Leu Ser Thr Glu Leu Met Leu Ala Cys Thr Glu Ala Leu Ser Ser
 1395 1400 1405
 Ser Tyr Val Lys Lys Asn Thr His Pro Lys Val Pro Glu Arg Leu Pro
 1410 1415 1420
 Asp Met Ile Asn Asp Cys Arg Phe His Trp Gln Asp Val Asn Lys Glu
 1425 1430 1435 1440
 Asp Met Leu Ala Asp Glu Phe Arg Lys Tyr Lys Cys Tyr Glu Lys Asn
 1445 1450 1455
 Pro Val Ile Ala Leu Pro His Pro Ser Leu Ser Ala Ser Leu Cys Arg
 1460 1465 1470
 Ser Leu Ser Ala Thr Pro Leu Lys Ile Asn Leu His Gln Phe Leu Gly
 1475 1480 1485
 Ser Gly Ile Leu Ile Leu Arg Leu Asn His His Arg His Pro Ala Thr
 1490 1495 1500
 Gly Ala Ser Phe Ser Asp Ser Cys Cys Thr Cys Cys Pro Lys Leu Thr
 1505 1510 1515 1520
 Thr Glu Ala Ala Val Ala Ala Val Ala Ala His Gln His Gln His Gln
 1525 1530 1535
 Asn Gln Gln Gln Gln Pro Asp Tyr Ala Val Ile Thr Gly Leu Ile Glu
 1540 1545 1550
 Ile Leu Ser Arg Arg Ile Gln Lys Val Arg Glu Ser Ile Glu Ser Asn
 1555 1560 1565
 Lys Ser Val Met Leu Ser Leu Leu Thr Thr Leu Gly Phe Leu Ser Arg
 1570 1575 1580
 Phe Ile Asp Val Cys Gln Pro Gly Pro Ala Asp Pro Thr Arg Leu Leu
 1585 1590 1595 1600
 Ser Ala Ala Lys Ser Thr Glu Leu Phe Gly Thr Val Ser Met Leu Tyr
 1605 1610 1615
 Gly Cys Val Met Pro Met Gly Glu Cys Ile Pro Pro Arg Thr Thr Ala
 1620 1625 1630
 Leu Ala Ala Ser Thr Phe His Leu Tyr Val Ser Leu Ala Ser Leu Asp
 1635 1640 1645
 Val Asn Thr Phe Gln Glu Thr Leu Thr Val Glu Gly Pro Leu Ser Leu
 1650 1655 1660
 Lys Leu Leu Asp Val Met Thr Val Ile Leu Asn Cys Ser Leu Val Asn
 1665 1670 1675 1680
 Asp Gln Trp Thr Thr Asn Ser Glu Ser Cys Pro Met Leu Ile Asp Leu
 1685 1690 1695

Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp
 1700 1705 1710
 Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys
 1715 1720 1725
 Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val
 1730 1735 1740
 Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp
 1745 1750 1755 1760
 Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn
 1765 1770 1775
 Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala
 1780 1785 1790
 Gly Asn Lys Lys Asn Ala
 1795

<210> 49
 <211> 274
 <212> PRT
 <213> *Toxocara canis*

<400> 49
 Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val
 1 5 10 15
 Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val
 20 25 30
 Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys
 35 40 45
 Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln
 50 55 60
 Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr
 65 70 75 80
 Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Ser Ile Thr Leu Arg Ile
 85 90 95
 Leu His Arg Pro Glu Pro Ser Lys Leu Pro Asn Ile Tyr Leu Asn Ile
 100 105 110
 Gly Gln Asp Tyr Ala Glu Arg Val Leu Pro Ser Ile Thr Asn Glu Val
 115 120 125
 Leu Lys Ala Val Val Ala Gln Phe Asp Ala His Glu Met Ile Thr Gln
 130 135 140
 Arg Glu Ser Val Ser His Arg Val Ser Val Glu Leu Ser Glu Arg Ala
 145 150 155 160

Arg Gln Phe Gly Ile Leu Leu Asp Asp Ile Ala Ile Thr His Leu Ser
 165 170 175
 Phe Gly Arg Glu Phe Thr Glu Ala Val Glu Met Lys Gln Val Ala Gln
 180 185 190
 Gln Glu Ala Glu Lys Ala Arg Tyr Leu Val Glu Thr Ala Glu Gln Met
 195 200 205
 Lys Ile Ala Ala Ile Thr Thr Ala Glu Gly Asp Ala Gln Ala Ala Lys
 210 215 220
 Leu Leu Ala Gln Ala Phe Lys Asp Ala Gly Asp Gly Leu Ile Glu Leu
 225 230 235 240
 Arg Lys Ile Glu Ala Ala Glu Glu Ile Ala Glu Arg Met Ser Lys Thr
 245 250 255
 Arg Asn Val Ile Tyr Leu Pro Gly Asn Gln Asn Thr Leu Phe Asn Leu
 260 265 270
 Pro Ala

<210> 50
 <211> 402
 <212> PRT
 <213> Caenorhabditis elegans

<400> 50
 Met Glu Lys Tyr Lys Asn Glu Leu Glu Ile Phe Lys Arg Met Tyr Phe
 1 5 10 15
 Lys Asn Tyr Pro Thr Ser Ser Lys Asp Glu Glu Ala Ala Ala Val Ile
 20 25 30
 Gln Lys Gly Gly Glu Phe Ile Gln Glu Ile Leu Pro Thr Ile Ile Ser
 35 40 45
 Thr Ser Arg Ala Tyr Asp Thr Asn Gln Lys Ala Leu Leu Leu Ala Glu
 50 55 60
 Gly Gly Lys Met Tyr Asn Val Leu Glu Asp Tyr Asn Glu Thr Ala Glu
 65 70 75 80
 Lys Met Leu Ser Lys Ser Val Arg Met Asn Pro Lys Asn Ala Asp Ala
 85 90 95
 Trp His Glu Leu Gly Leu Cys Val Met Lys Arg Arg Asp Leu Glu Phe
 100 105 110
 Ala Gln Ser Cys Phe Lys Ile Ala Leu Gly Ile Ser Lys Thr Ala Pro
 115 120 125
 Ile Leu Thr Ser Leu Ala Val Ala Met Arg Leu Val Ala Leu Glu His

130	135	140
Pro Glu Pro Ala Gln Ala Glu Ile Arg Thr Lys Ala Met Glu Leu Ile 145 150 155 160		
Ile Glu Ala Arg Arg Leu Asp Ser Ala Tyr Gly Pro Ala Asn Ile Ala 165 170 175		
Phe Ala Thr Gly Leu Phe Tyr Cys Phe Phe Ser Thr Ala Lys Val Glu 180 185 190		
Leu Lys Phe Leu Asp Lys Val Ile Glu Asn Tyr Lys Lys Ala Leu Glu 195 200 205		
Cys Glu Leu Ser Arg Thr Asp Pro Gln Val Tyr Ile Asn Met Ala Thr 210 215 220		
Cys Leu Lys Phe Met Glu Lys Tyr Asp Glu Ala Leu Ala Val Leu Gln 225 230 235 240		
Lys Ala Val Glu Tyr Asp Pro Arg Asn Glu Leu Glu Thr Arg Glu Lys 245 250 255		
Leu Ala Ser Phe Val Ser Tyr Leu Ser Lys Phe Thr Asp Ala Ile Gln 260 265 270		
Lys Lys Gly Lys Met Lys Ala Lys Arg Met Gln Glu Met Ile Asn Glu 275 280 285		
Leu Lys Lys Ser Ser Asp Gly Phe Arg Ala Lys Ile Ile Gly Asn Ile 290 295 300		
Gly His Asp Glu Thr Ile Pro Val Ala Leu Val Gly Val Asp Ala Ala 305 310 315 320		
Gly Glu Val Tyr Gly Ile Thr Ile Tyr Asn Cys Leu Ser Asn Phe Gly 325 330 335		
Phe Val Ile Gly Asp Thr Val Thr Ile Ala Lys Pro Asp Phe Arg Glu 340 345 350		
Ile Lys Asn Leu Thr Ile Pro Ser Asp Pro Glu Ile His Val Asp Ser 355 360 365		
Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly 370 375 380		
Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln 385 390 395 400		
Thr Lys		

<210> 51
 <211> 711
 <212> PRT

<213> Homo sapiens

<400> 51

Met	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Thr	Gln	Cys	Leu	Gly	Val	
1				5					10					15		
Pro	Gly	Gln	Arg	Ser	Pro	Leu	Asn	Asp	Phe	Gln	Val	Leu	Arg	Gly	Thr	
			20					25					30			
Glu	Leu	Gln	His	Leu	Leu	His	Ala	Val	Val	Pro	Gly	Pro	Trp	Gln	Glu	
		35					40					45				
Asp	Val	Ala	Asp	Ala	Glu	Glu	Cys	Ala	Gly	Arg	Cys	Gly	Pro	Leu	Met	
	50					55					60					
Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Val	Ser	Ser	His	Gly	Cys	Gln	Leu	
65					70					75					80	
Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	Arg	Ser	Gly	
				85					90					95		
Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met	
		100						105					110			
Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	
		115					120					125				
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	
	130					135					140					
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	
145					150					155					160	
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	
				165					170					175		
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	
			180					185					190			
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	
		195					200					205				
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	
	210					215					220					
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	
225					230					235					240	
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	
				245					250					255		
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	
			260					265					270			
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	
		275					280					285				

Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys
 370 375 380
 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His
 385 390 395 400
 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu
 405 410 415
 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr
 420 425 430
 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys
 435 440 445
 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590

Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 52
 <211> 711
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
 1 5 10 15
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
 85 90 95
 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110
 Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
 115 120 125
 Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
 130 135 140

Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	145	150	155	160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	165	170		175
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	180	185		190
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	195	200		205
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	210	215		220
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250		255
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	260	265		270
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	275	280		285
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	290	295	300	
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	305	310	315	320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	325	330		335
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	340	345		350
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	355	360		365
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	370	375	380	
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	385	390	395	400
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	405	410		415
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	420	425		430
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	435	440		445

Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Phe Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 53
 <211> 711
 <212> PRT
 <213> Homo sapiens

<400> 53

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
210 215 220

Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
225 230 235 240

Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
245 250 255

Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
260 265 270

Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
275 280 285

Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys

290		295		300
Gln Arg Trp Asp Ala	Gln Ile Pro His	Gln His Arg Phe Thr Pro Glu		
305	310	315		320
Lys Tyr Ala Cys	Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp			
	325	330		335
Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala				
	340	345		350
Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln				
	355	360		365
Asp Cys Tyr His Gly Ala	Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys			
	370	375	380	
Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His				
	385	390	395	400
Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu				
	405	410		415
Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr				
	420	425		430
Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys				
	435	440		445
Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln				
	450	455	460	
Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser				
	465	470	475	480
Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val				
	485	490		495
Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val				
	500	505		510
Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His				
	515	520	525	
Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn				
	530	535	540	
Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met				
	545	550	555	560
Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg				
	565	570		575
Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu				
	580	585		590
Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly				

595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 54
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 54
 Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln
 1 5 10 15
 Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser
 20 25 30
 Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile
 35 40 45
 Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly
 50 55 60
 Gly Leu Ser Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Gln
 65 70 75 80
 Tyr Met Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn
 85 90 95
 Pro Asp Gly Asp Pro Gly Gly Pro Trp Cys His Thr Thr Asp Pro Ala
 100 105 110
 Val Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Val Ala Ala Cys
 115 120 125
 Val Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu
 130 135 140

Ser	Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His		
145					150				155					160			
Pro	Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr		
				165				170						175			
Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp		
			180					185					190				
Pro	Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu		
		195					200					205					
Ala	Gln	Pro	Arg	Gln	Glu	Ala	Thr	Ser	Val	Ser	Cys	Phe	Arg	Gly	Lys		
	210					215					220						
Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro		
225					230				235					240			
Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro		
				245				250						255			
Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro		
			260				265						270				
Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg		
		275					280					285					
Val	Gly	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro		
	290					295					300						
Gln	Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser		
305					310					315				320			
Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Gly	Ser	Ala	Glu	Thr	Pro		
				325					330					335			
His	Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu		
			340					345					350				
Glu	Asn	Phe	Cys	Gln	Thr	Gln	Met	Gly	Ile	Ala	Met	Gly	Pro	Gly	Ala		
		355					360				365						
Thr	Arg	Trp	Thr	Gln	Gly	Pro	His	Ser	Thr	Thr	Val	Pro	Cys	Asp	Ala		
	370					375					380						
Ala	Leu	Met	Thr	Ser	Arg	His	Gln	Ser	Trp	Thr	Pro	Gln	Thr	Arg	Cys		
385					390					395				400			
Ser	Leu	Arg	Ser	Val	Ala	Arg	Gly	Trp	Ile	Gly	Trp	Ile	Ser	Val	Val		
				405				410						415			
Pro	Ser	Cys	Ala	Trp	Leu	Gly	Ala	Ile	Arg	Ala	Thr	His	Pro	Gly	Gln		
			420					425					430				
Ser	Ala	Cys	Gly	Ile	Gly	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu		
		435					440					445					

Val Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys
 450 455 460

His Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln
 465 470 475 480

Asn Pro Gln His Gly Glu Pro Gly Leu Gln Arg Val Pro Val Ala Lys
 485 490 495

Met Leu Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu
 500 505 510

Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro
 515 520 525

Glu

<210> 55

<211> 716

<212> PRT

<213> Mus musculus

<400> 55

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Val Gln Cys Ser Arg Ala
 1 5 10 15

Leu Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Leu Phe Arg Gly Thr
 20 25 30

Glu Leu Arg Asn Leu Leu His Thr Ala Val Pro Gly Pro Trp Gln Glu
 35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Arg Arg Cys Gly Pro Leu Leu
 50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Met Ser Ser His Gly Cys Gln Leu
 65 70 75 80

Leu Pro Trp Thr Gln His Ser Leu His Thr Gln Leu Tyr His Ser Ser
 85 90 95

Leu Cys His Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110

Asp Asn Gly Val Ser Tyr Arg Gly Thr Val Ala Arg Thr Ala Gly Gly
 115 120 125

Leu Pro Cys Gln Ala Trp Ser Arg Arg Phe Pro Asn Asp His Lys Tyr
 130 135 140

Thr Pro Thr Pro Lys Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160

Asp Gly Asp Pro Arg Gly Pro Trp Cys Tyr Thr Thr Asn Arg Ser Val
 165 170 175

Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Thr	Cys	Arg	Glu	Ala	Val	Cys	Val	180	185	190	
Leu	Cys	Asn	Gly	Glu	Asp	Tyr	Arg	Gly	Glu	Val	Asp	Val	Thr	Glu	Ser	195	200	205	
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Ser	His	Pro	210	215	220	
Phe	Gln	Pro	Glu	Lys	Phe	Leu	Asp	Lys	Asp	Leu	Lys	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250	255	
Asn	Val	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Ser	Cys	Gly	Pro	Asn	Leu	260	265	270	
Pro	Pro	Thr	Val	Lys	Gly	Ser	Lys	Ser	Gln	Arg	Arg	Asn	Lys	Gly	Lys	275	280	285	
Ala	Leu	Asn	Cys	Phe	Arg	Gly	Lys	Gly	Glu	Asp	Tyr	Arg	Gly	Thr	Thr	290	295	300	
Asn	Thr	Thr	Ser	Ala	Gly	Val	Pro	Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ser	305	310	315	320
Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	325	330	335	
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	340	345	350	
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro	355	360	365	
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly	370	375	380	
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	385	390	395	400
Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr	405	410	415	
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp	420	425	430	
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu	435	440	445	
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser	450	455	460	
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg	465	470	475	480

Val Asp Lys Ser Asn Lys Leu Arg Val Val Gly Gly His Pro Gly Asn
 485 490 495
 Ser Pro Trp Thr Val Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys
 500 505 510
 Gly Gly Ser Leu Val Lys Glu Gln Trp Val Leu Thr Ala Arg Gln Cys
 515 520 525
 Ile Trp Ser Cys His Glu Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly
 530 535 540
 Thr Ile Asn Gln Asn Pro Gln Pro Gly Glu Ala Asn Leu Gln Arg Val
 545 550 555 560
 Pro Val Ala Lys Ala Val Cys Gly Pro Ala Gly Ser Gln Leu Val Leu
 565 570 575
 Leu Lys Leu Glu Arg Pro Val Ile Leu Asn His His Val Ala Leu Ile
 580 585 590
 Cys Leu Pro Pro Glu Gln Tyr Val Val Pro Pro Gly Thr Lys Cys Glu
 595 600 605
 Ile Ala Gly Trp Gly Glu Ser Ile Gly Thr Ser Asn Asn Thr Val Leu
 610 615 620
 His Val Ala Ser Met Asn Val Ile Ser Asn Gln Glu Cys Asn Thr Lys
 625 630 635 640
 Tyr Arg Gly His Ile Gln Glu Ser Glu Ile Cys Thr Gln Gly Leu Val
 645 650 655
 Val Pro Val Gly Ala Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys
 660 665 670
 Tyr Thr His Asp Cys Trp Val Leu Gln Gly Leu Ile Ile Pro Asn Arg
 675 680 685
 Val Cys Ala Arg Pro Arg Trp Pro Ala Ile Phe Thr Arg Val Ser Val
 690 695 700
 Phe Val Asp Trp Ile Asn Lys Val Met Gln Leu Glu
 705 710 715

<210> 56
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15

Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu

20	25	30
Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Val Thr Cys Asp		
35	40	45
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln		
50	55	60
Phe Ser Cys Pro Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly		
65	70	75
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln		
85	90	95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys		
100	105	110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn His Val Ala Cys Thr		
115	120	125
Arg Ile Tyr Glu Lys Val Glu		
130	135	

<210> 57
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 57
Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30
Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60
Phe Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
100 105 110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125
Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 58
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15
 Arg Gly Phe Asp Glu Tyr Val Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Arg Lys Met Asp Thr Ile Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60
 Phe Ser Cys Thr Leu Gly Glu Asn Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95
 His Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Arg Arg Lys Leu Lys
 100 105 110
 Asp Gly Lys Leu Val Val Asp Cys Val Met Asn Ser Val Thr Cys Thr
 115 120 125
 Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 59
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Leu Asp Ser
 1 5 10 15
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Arg Asn Leu Thr Thr Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60
 Phe Ser Cys Thr Leu Gly Asp Glu Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln

	85		90		95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys	100		105		110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr	115		120		125
Arg Ile Tyr Glu Lys Val Glu	130		135		

<210> 60
 <211> 135
 <212> PRT
 <213> Bos taurus

<400> 60	
Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser	15
1	5
Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu	30
20	25
Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp	45
35	40
Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln	60
50	55
Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly	80
65	70
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln	95
85	90
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu	110
100	105
Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr	125
115	120
Arg Val Tyr Glu Lys Val Glu	135
130	

<210> 61
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 61	
Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr	15
1	5
Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg	30
20	25

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45
 Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60
 Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 55 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
 100 105 110
 Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
 130 135 140
 Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160
 Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175
 Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
 195 200 205
 Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
 210 215 220
 Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
 225 230 235 240
 Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
 245 250 255
 Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
 260 265

<210> 62
 <211> 265
 <212> PRT
 <213> Rattus norvegicus

<400> 62
 Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15
 Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg

20					25					30						
Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp	Asp	Glu	Gln	
35					40					45						
Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys	Pro	Asn	Val	Cys	
50					55					60						
Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln	
65					70					75					80	
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala	
85					90					95						
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	Arg	Leu	Lys	His	Gly	Pro	Asp	
100					105					110						
Ala	Pro	Ala	Leu	Tyr	Ser	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp	
115					120					125						
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ser	Gly	
130					135					140						
Phe	Leu	Tyr	Ile	Phe	His	Cys	Ile	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg	
145					150					155					160	
Val	Val	Ala	Cys	Ser	Val	Gln	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr	
165					170					175						
Ile	Ser	Arg	Pro	Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Val	
180					185					190						
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Ala	Tyr	Leu	
195					200					205						
Val	Gly	Lys	Arg	Cys	Met	Glu	Val	Phe	Arg	Pro	Arg	Arg	Gln	Lys	Thr	
210					215					220						
Ser	Arg	Arg	His	Gln	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Ile	Ser	
225					230					235					240	
Lys	Gly	His	Pro	Gln	Asp	Glu	Ser	Thr	Val	Leu	Thr	Lys	Ala	Gly	Met	
245					250					255						
Ala	Thr	Val	Asp	Ala	Gly	Val	Tyr	Pro								
260					265											

<210> 63
 <211> 266
 <212> PRT
 <213> Mus musculus

<400> 63
 Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15

Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Asp Gln
 35 40 45
 Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60
 Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn
 100 105 110
 Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly
 130 135 140
 Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160
 Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175
 Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu
 195 200 205
 Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala
 210 215 220
 Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser
 225 230 235 240
 Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly
 245 250 255
 Met Ala Thr Val Asp Ala Gly Val Tyr Pro
 260 265

<210> 64

<211> 273

<212> PRT

<213> Homo sapiens

<400> 64

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 35 40 45
 Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
 50 55 60
 Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
 100 105 110
 Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
 130 135 140
 Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
 145 150 155 160
 Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
 165 170 175
 Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
 195 200 205
 Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
 210 215 220
 Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
 225 230 235 240
 Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
 245 250 255
 Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
 260 265 270

Leu

<210> 65
 <211> 273
 <212> PRT
 <213> Homo sapiens

<220>

<221> VARIANT

<222> (41)

<223> Wherein Xaa is any amino acid.

<400> 65

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
195 200 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
210 215 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
225 230 235 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
245 250 255

Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
260 265 270

Leu

<210> 66
<211> 434
<212> PRT
<213> Homo sapiens

<400> 66

Ala Lys Gln Gln Leu Asn Leu Arg Thr His Met Ala Asp Glu Asn Lys
1 5 10 15

Asn Glu Tyr Ala Ala Gln Leu Gln Asn Phe Asn Gly Glu Gln His Lys
20 25 30

His Phe Tyr Val Val Ile Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met
35 40 45

Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala
50 55 60

Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly
65 70 75 80

Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln Met
85 90 95

Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro
100 105 110

Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly Thr
115 120 125

Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr Thr
130 135 140

Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys
145 150 155 160

Pro Gln Ser Pro Pro Leu Thr Pro Thr Ser Leu Phe Thr Ser Ser Thr
165 170 175

Pro Asn Gly Ser Gln Phe Leu Thr Phe Ser Ile Glu Pro Val His Tyr
180 185 190

Cys Met Asn Glu Ile Lys Thr Gly Lys Pro Arg Ile Pro Ser Phe Arg
195 200 205

Ser Leu Lys Arg Gly Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro
210 215 220

Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn
225 230 235 240

Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met

	245		250		255
Lys Asp Val Tyr Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu					
	260		265		270
Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met					
	275		280		285
Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr					
	290		295		300
Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val					
305		310		315	320
Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn					
	325		330		335
Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe					
	340		345		350
Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys					
	355		360		365
Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met					
	370		375		380
Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly					
385		390		395	400
Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr					
	405		410		415
Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser Lys Gly Ala Val Thr					
	420		425		430

Tyr Ile

<210> 67
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 67
 Met Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe
 1 5 10 15
 Ala Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu
 20 25 30
 Gly Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln
 35 40 45
 Met Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe
 50 55 60

Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly
 65 70 75 80
 Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr
 85 90 95
 Thr Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro
 100 105 110
 Lys Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro Pro Glu Gln Arg
 115 120 125
 Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn Arg Glu Leu Gln
 130 135 140
 Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met Lys Asp Val Tyr
 145 150 155 160
 Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu Gln Pro Lys Leu
 165 170 175
 Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met Glu Ile His Lys
 180 185 190
 Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr Gly Gly Arg Gly
 195 200 205
 Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val Thr Gln Gly Arg
 210 215 220
 Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn Gln Glu Val Arg
 225 230 235 240
 Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe Asp Asp Glu Phe
 245 250 255
 Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys Lys Ala Ile Tyr
 260 265 270
 Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met Lys Glu Gly Glu
 275 280 285
 Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala
 290 295 300
 Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp
 305 310 315 320
 Val Thr Leu Glu Lys Asn Ser Lys Gly Ser
 325 330

<210> 68

<211> 592

<212> PRT

<213> Homo sapiens

<400> 68

Met	Ser	Trp	Gly	Thr	Glu	Leu	Trp	Asp	Gln	Phe	Asp	Asn	Leu	Glu	Lys	1	5	10	15
His	Thr	Gln	Trp	Gly	Ile	Asp	Ile	Leu	Glu	Lys	Tyr	Ile	Lys	Phe	Val	20	25	30	
Lys	Glu	Arg	Thr	Glu	Ile	Glu	Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn	35	40	45	
Leu	Ser	Lys	Lys	Tyr	Gln	Pro	Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu	50	55	60	
Tyr	Lys	Tyr	Thr	Ser	Cys	Lys	Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met	65	70	75	80
Asn	Asp	Tyr	Ala	Gly	Gln	His	Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	85	90	95	
Gln	Ile	Ile	Val	Asp	Leu	Ala	Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	100	105	110	
Arg	Lys	Ser	Asn	Phe	His	Asp	Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	115	120	125	
Thr	Cys	Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	130	135	140	
Cys	Lys	Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	145	150	155	160
Asp	Ile	Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	165	170	175	
Gln	Ile	Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	180	185	190	
Ile	Leu	Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	195	200	205	
Ile	Pro	Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	210	215	220	
Val	Arg	Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	225	230	235	240
Val	Ile	Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	245	250	255	
Glu	Ser	Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	260	265	270	
Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	275	280	285	
Gln	Pro	Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	290	295	300	

Gly	Glu	Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys		
305					310					315						320	
Leu	Trp	Pro	Phe	Ile	Lys	Lys	Asn	Lys	Ser	Pro	Lys	Gln	Gln	Lys	Glu		
				325					330						335		
Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile		
			340					345					350				
His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala		
		355					360					365					
Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys		
	370					375					380						
Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met		
385					390					395					400		
Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn		
				405					410					415			
Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val		
			420					425					430				
Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala		
		435					440					445					
Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Asn	Glu	Gln	Ala		
	450					455					460						
Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn		
465					470				475						480		
Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu		
				485					490					495			
Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp		
			500					505					510				
Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala		
		515					520					525					
Leu	Tyr	Thr	Phe	Glu	Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu		
	530					535					540						
Gly	Glu	Thr	Leu	Tyr	Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr		
545					550					555					560		
Arg	Ile	Arg	Arg	Asn	Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr		
				565					570					575			
Val	Glu	Val	Cys	Leu	Asp	Lys	Asn	Ala	Lys	Gly	Ala	Lys	Thr	Tyr	Ile		
			580					585					590				

<210> 69
 <211> 679
 <212> PRT
 <213> Homo sapiens

<400> 69

Leu Trp Asn Gly Gly Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg
 1 5 10 15

Ser Cys Glu Pro Glu Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser
 20 25 30

Arg Gly Ser Arg Gly Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu
 35 40 45

Pro Arg Pro Pro Arg Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser
 50 55 60

Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr
 65 70 75 80

Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu
 85 90 95

Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser
 100 105 110

Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys
 115 120 125

Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp
 130 135 140

Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile
 145 150 155 160

Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys
 165 170 175

Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys
 180 185 190

Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp Cys Lys
 195 200 205

Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala Asp Ile
 210 215 220

Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala Gln Ile
 225 230 235 240

Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser Ile Leu
 245 250 255

Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His Ile Pro

260										265										270																																		
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg																																							
		275					280					285																																										
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile																																							
	290					295					300																																											
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser																																							
305					310					315					320																																							
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser																																							
				325					330					335																																								
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro																																							
			340					345					350																																									
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu																																							
		355					360					365																																										
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp																																							
	370					375					380																																											
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His																																							
385					390					395				400																																								
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro																																							
				405					410					415																																								
Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg																																							
		420					425					430																																										
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser																																							
		435					440					445																																										
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe																																							
	450					455					460																																											
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val																																							
465					470				475					480																																								
Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala																																							
				485					490					495																																								
Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp																																							
			500					505					510																																									
Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu																																							
		515					520					525																																										
Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val																																							
	530					535					540																																											
Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly																																							
545					550				555					560																																								
Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp																																							

	565		570		575
Arg Glu Ser	Pro Asp Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser				
	580		585		590
Glu Met Lys Val Leu Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu					
	595		600		605
Glu Pro Leu Pro Ala Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu					
	610		615		620
Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr					
	625		630		635
Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn					
	645		650		655
Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu					
	660		665		670
Asp Lys Asn Ala Lys Asp Ser					
	675				

<210> 70
 <211> 674
 <212> PRT
 <213> Homo sapiens

<400> 70
Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu
1 5 10 15
Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly
20 25 30
Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg
35 40 45
Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu
50 55 60
Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr Gln Trp Gly Ile Asp
65 70 75 80
Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu Arg Thr Glu Ile Glu
85 90 95
Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser Lys Lys Tyr Gln Pro
100 105 110
Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys Tyr Thr Ser Cys Lys
115 120 125
Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp Tyr Ala Gly Gln His
130 135 140

Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile	Ile	Val	Asp	Leu	Ala	145	150	155	160
Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys	Ser	Asn	Phe	His	Asp	165	170		175
Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys	Trp	Lys	Gln	Leu	Glu	180	185		190
Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	Glu	Ala	Asp	Arg	Ala	195	200		205
Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	Asn	Val	Thr	Lys	Ala	210	215		220
Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	Arg	His	Gln	Met	Ala	225	230	235	240
Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	Gln	Lys	Phe	Asn	His	245	250		255
Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	Asn	Ile	Phe	Gln	Lys	260	265		270
Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	Met	Gly	Glu	Ser	Met	275	280		285
Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	Pro	Ile	Ile	Gly	Lys	290	295	300	
Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	Ile	Asp	Gln	Lys	Asn	305	310	315	320
Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	Gly	Phe	Glu	Pro	Pro	325	330		335
Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	Met	Lys	Arg	Thr	Val	340	345		350
Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	Gly	Lys	Pro	Asp	Leu	355	360		365
Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp	Pro	Phe	Ile	Lys	Lys	370	375	380	
Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His	Gln	Pro	Pro	Pro	Pro	385	390	395	400
Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro	Asn	Gly	Pro	Gln	Ser	405	410		415
Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	420	425		430
Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	435	440		445

Ser Leu Lys Leu Gly Ala Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro
 450 455 460

Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val Asp Glu Leu Asn Lys
 465 470 475 480

Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala Ile Thr Lys Met Lys
 485 490 495

Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp Pro Ala Ser Leu Asp
 500 505 510

His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu Lys Leu Arg Val Glu
 515 520 525

Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val Glu Gly Arg Leu Pro
 530 535 540

Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln
 545 550 555 560

Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp
 565 570 575

Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser Glu Met Lys Val Leu
 580 585 590

Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala
 595 600 605

Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly
 610 615 620

Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp
 625 630 635 640

Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly
 645 650 655

Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu Asp Lys Asn Ala Lys
 660 665 670

Asp Ser

<210> 71
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1 5 10 15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
 20 25 30

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240

His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255

Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270

Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300

His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320

Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335

Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350
 Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro Leu
 355 360 365
 Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala Leu
 370 375 380
 Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 385 390 395 400
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp Thr
 405 410 415
 Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu Pro
 420 425 430
 Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 435 440 445
 His Asp Thr Ala Gln Asp Ser Leu Leu
 450 455

<210> 72
 <211> 455
 <212> PRT
 <213> Mus musculus

<400> 72
 Met Ser Pro Thr Leu Asp Asp Gln Ser Pro Met Glu Ile Arg Cys Thr
 1 5 10 15
 Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg Met Glu Leu Gly Asp Gln
 20 25 30
 Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp Cys Cys Leu Gln Arg Gly
 35 40 45
 Cys Val Ile Leu Gly Val Leu Gly Leu Leu Ala Gly Ala Gly Ile Ala
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro Ala Ala Ser Pro Ser Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Glu Glu Glu Met Thr Leu Asn Cys Pro Gly Val
 85 90 95
 Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Gly Glu Asp Leu Leu Gln Val Gln Val Arg Ala Arg
 115 120 125
 Pro Asp Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly

130	135	140
Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys		
145	150	155 160
Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala		
	165	170 175
Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro		
	180	185 190
Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu		
	195	200 205
Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val		
	210	215 220
Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg		
	225	230 235 240
His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala		
	245	250 255
Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg		
	260	265 270
Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly		
	275	280 285
Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn		
	290	295 300
His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe		
	305	310 315 320
Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe		
	325	330 335
Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro		
	340	345 350
Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu		
	355	360 365
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu		
	370	375 380
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala		
	385	390 395 400
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr		
	405	410 415
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro		
	420	425 430
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile		

435 440 445
 His Asp Thr Val Gln Val Arg
 450 455

 <210> 73
 <211> 445
 <212> PRT
 <213> Mus musculus

 <400> 73
 Met Glu Ile Arg Cys Thr Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg
 1 5 10 15
 Met Glu Leu Gly Asp Gln Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp
 20 25 30
 Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu Gly Leu Leu
 35 40 45
 Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro
 50 55 60
 Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln Glu Glu Glu Met Thr
 65 70 75 80
 Leu Asn Cys Pro Gly Val Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu
 85 90 95
 Pro Lys Thr Val Ser Phe Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln
 100 105 110
 Val Gln Val Arg Ala Arg Pro Asp Trp Leu Leu Val Cys His Glu Gly
 115 120 125
 Trp Ser Pro Ala Leu Gly Met His Ile Cys Lys Ser Leu Gly His Ile
 130 135 140
 Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp Ile Lys Leu Asn
 145 150 155 160
 Arg Ser Gln Glu Phe Ala Gln Leu Ser Ala Arg Pro Gly Gly Leu Val
 165 170 175
 Glu Glu Ala Trp Lys Pro Ser Ala Asn Cys Pro Ser Gly Arg Ile Val
 180 185 190
 Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile
 195 200 205
 Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser
 210 215 220
 Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala Pro
 225 230 235 240

His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu Ser
 245 250 255
 Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly Ala
 260 265 270
 Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His Pro
 275 280 285
 Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln Leu
 290 295 300
 Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro
 305 310 315 320
 Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser Gly
 325 330 335
 Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu Gln
 340 345 350
 Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser Cys
 355 360 365
 Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr Leu
 370 375 380
 Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 385 390 395 400
 Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp Gly
 405 410 415
 Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val Ala
 420 425 430
 Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
 435 440 445

<210> 74

<211> 398

<212> PRT

<213> Homo sapiens

<400> 74

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1 5 10 15
 Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
 20 25 30
 Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240

His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255

Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270

Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300

His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320

Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335

Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350

Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu
 355 360 365

Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro
 370 375 380

His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly
 385 390 395

<210> 75
 <211> 311
 <212> PRT
 <213> Mus musculus

<400> 75
 Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys
 1 5 10 15

Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
 20 25 30

Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
 35 40 45

Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu
 50 55 60

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val
 65 70 75 80

Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg
 85 90 95

His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala
 100 105 110

Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg
 115 120 125

Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly
 130 135 140

Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 145 150 155 160

His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe
 165 170 175

Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe
 180 185 190

Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro
 195 200 205

Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu
 210 215 220

Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu

225	230	235	240
Thr His Arg Met	Leu Cys Ala Gly Tyr	Leu Asp Gly Arg Ala	Asp Ala
	245	250	255
Cys Gln Gly Asp	Ser Gly Gly Pro	Leu Val Cys Pro	Ser Gly Asp Thr
	260	265	270
Trp His Leu Val	Gly Val Val Ser	Trp Gly Arg Gly	Cys Ala Glu Pro
	275	280	285
Asn Arg Pro Gly	Val Tyr Ala Lys	Val Ala Glu Phe	Leu Asp Trp Ile
	290	295	300
His Asp Thr Val	Gln Val Arg		
305	310		

<210> 76
 <211> 199
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reprolysin
 family zinc protease Consensus Sequence

<400> 76

Lys Tyr Ile Glu	Leu Phe Ile Val	Val Asp His Gly	Met Phe Thr Lys
1	5	10	15
Tyr Gly Ser Asp	Leu Asn Lys Ile	Arg Gln Arg Val	His Gln Ile Val
	20	25	30
Asn Leu Val Asn	Glu Ile Tyr Arg	Pro Leu Asn Ile	Arg Val Val Leu
	35	40	45
Val Gly Leu Glu	Ile Trp Ser Asp	Gly Asp Lys Ile	Thr Val Gln Gly
	50	55	60
Asp Ala Asn Asp	Thr Leu His Arg	Phe Leu Glu Trp	Arg Glu Thr Asp
	65	70	75
Leu Leu Lys Arg	Lys Ser His Asp	Asn Ala Gln Leu	Leu Thr Gly Ile
	85	90	95
Asp Phe Asp Gly	Asn Thr Ile Gly	Ala Ala Tyr Val	Gly Gly Met Cys
	100	105	110
Ser Pro Lys Arg	Ser Val Gly Val	Val Gln Asp His	Ser Pro Ile Val
	115	120	125
Leu Leu Val Ala	Val Thr Met Ala	His Glu Leu Gly	His Asn Leu Gly
	130	135	140
Met Thr His Asp	Asp Ile Asn Lys	Cys Thr Cys Glu	Gly Gly Gly Gly
	145	150	155
			160

Cys Ile Met Asn Pro Val Ala Ser Ser Ser Pro Gly Lys Lys Phe Ser
165 170 175

Asn Cys Ser Met Asp Asp Tyr Gln Gln Phe Leu Thr Lys Gly Lys Pro
180 185 190

Gln Cys Leu Leu Asn Lys Pro
195

<210> 77
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 Consensus Sequence

<400> 77
Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly
1 5 10 15

Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly
20 25 30

Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln
35 40 45

Pro Cys Pro
50

<210> 78
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 domain Consensus Sequence

<400> 78
Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly
1 5 10 15

Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro
20 25 30

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys
35 40 45

<210> 79
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reprolysin
 family propeptide Consensus Sequence

<400> 79
 His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr
 1 5 10 15
 Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln
 20 25 30
 Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala
 35 40 45
 Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu
 50 55 60
 Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu
 65 70 75 80
 His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys
 85 90 95
 Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile
 100 105 110
 Arg Ser Pro Ser Pro
 115

<210> 80
 <211> 751
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Alpha-2-macroglobulin family Consensus Sequence

<400> 80
 Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu Ser Trp
 1 5 10 15
 Leu Trp Glu Val Glu Glu Val Asp Arg Ser Pro Val Leu Thr Val Asn
 20 25 30
 Ile Thr Leu Pro Asp Ser Ile Thr Thr Trp Glu Ile Leu Ala Val Ser
 35 40 45
 Leu Ser Asn Thr Lys Gly Leu Cys Val Ala Asp Pro Val Glu Leu Thr
 50 55 60

Val Phe Gln Asp Phe Phe Leu Glu Leu Arg Leu Pro Tyr Ser Val Val
 65 70 75 80
 Arg Gly Glu Gln Val Glu Leu Arg Ala Val Leu Tyr Asn Tyr Leu Pro
 85 90 95
 Ser Gln Asp Ile Lys Val Val Val Gln Leu Glu Val Glu Pro Leu Cys
 100 105 110
 Gln Ala Gly Phe Cys Ser Leu Ala Thr Gln Arg Thr Arg Ser Ser Gln
 115 120 125
 Ser Val Arg Pro Lys Ser Leu Ser Ser Val Ser Phe Pro Val Val Val
 130 135 140
 Val Pro Leu Ala Ser Gly Leu Ser Leu Val Glu Val Val Ala Ser Val
 145 150 155 160
 Pro Glu Phe Phe Val Lys Asp Ala Val Val Lys Thr Leu Lys Val Glu
 165 170 175
 Pro Glu Gly Ala Arg Lys Glu Glu Thr Val Ser Ser Leu Leu Leu Pro
 180 185 190
 Pro Glu His Leu Gly Gly Gly Leu Glu Val Ser Glu Val Pro Ala Leu
 195 200 205
 Lys Leu Pro Asp Asp Val Pro Asp Thr Glu Ala Glu Ala Val Ile Ser
 210 215 220
 Val Gln Gly Asp Pro Val Ala Gln Ala Ile Gln Asn Thr Leu Ser Gly
 225 230 235 240
 Glu Gly Leu Asn Asn Leu Leu Arg Leu Pro Ser Gly Cys Gly Glu Gln
 245 250 255
 Asn Met Ile Tyr Met Ala Pro Thr Val Tyr Val Leu His Tyr Leu Asp
 260 265 270
 Glu Thr Trp Gln Trp Glu Lys Pro Gly Thr Lys Lys Lys Gln Lys Ala
 275 280 285
 Ile Asp Leu Ile Asn Lys Gly Tyr Gln Arg Gln Leu Asn Tyr Arg Lys
 290 295 300
 Ala Asp Gly Ser Tyr Ala Ala Phe Leu His Arg Ala Ser Ser Thr Trp
 305 310 315 320
 Leu Thr Ala Phe Val Leu Lys Val Phe Ser Gln Ala Arg Asn Tyr Val
 325 330 335
 Phe Ile Asp Glu Glu His Ile Cys Gly Ala Val Lys Trp Leu Ile Leu
 340 345 350
 Asn Gln Gln Lys Asp Asp Gly Val Phe Arg Glu Ser Gly Pro Val Ile
 355 360 365

His Asn Glu Met Lys Gly Gly Val Gly Asp Asp Ala Glu Val Glu Val
 370 375 380
 Thr Leu Thr Ala Phe Ile Thr Ile Ala Leu Leu Glu Ala Lys Leu Val
 385 390 395 400
 Cys Ile Ser Pro Val Val Ala Asn Ala Leu Ser Ile Leu Lys Ala Ser
 405 410 415
 Asp Tyr Leu Leu Glu Asn Tyr Ala Asn Gly Gln Arg Val Tyr Thr Leu
 420 425 430
 Ala Leu Thr Ala Tyr Ala Leu Ala Leu Ala Gly Val Leu His Lys Leu
 435 440 445
 Lys Glu Ile Leu Lys Ser Leu Lys Glu Glu Leu Tyr Lys Ala Leu Val
 450 455 460
 Lys Gly His Trp Glu Arg Pro Gln Lys Pro Lys Asp Ala Pro Gly His
 465 470 475 480
 Pro Tyr Ser Pro Gln Pro Gln Ala Ala Ala Val Glu Met Thr Ser Tyr
 485 490 495
 Ala Leu Leu Ala Leu Leu Thr Leu Leu Pro Phe Pro Lys Val Glu Met
 500 505 510
 Ala Pro Lys Val Val Lys Trp Leu Thr Glu Gln Gln Tyr Tyr Gly Gly
 515 520 525
 Gly Phe Gly Ser Thr Gln Asp Thr Val Met Ala Leu Gln Ala Leu Ser
 530 535 540
 Lys Tyr Gly Ile Ala Thr Pro Thr His Lys Glu Lys Asn Leu Ser Val
 545 550 555 560
 Thr Ile Gln Ser Pro Ser Gly Ser Phe Lys Ser His Phe Gln Ile Leu
 565 570 575
 Asn Asn Asn Ala Phe Leu Leu Arg Pro Val Glu Leu Pro Leu Asn Glu
 580 585 590
 Gly Phe Thr Val Thr Ala Lys Val Thr Gly Gln Gly Thr Leu Thr Leu
 595 600 605
 Val Thr Thr Tyr Arg Tyr Lys Val Leu Asp Lys Lys Asn Thr Phe Cys
 610 615 620
 Phe Asp Leu Lys Ile Glu Thr Val Pro Asp Thr Cys Val Glu Pro Lys
 625 630 635 640
 Gly Ala Lys Asn Ser Asp Tyr Leu Ser Ile Cys Thr Arg Tyr Ala Gly
 645 650 655
 Ser Arg Ser Asp Ser Gly Met Ala Ile Ala Asp Ile Ser Met Leu Thr
 660 665 670

Gly Phe Ile Pro Leu Lys Pro Asp Leu Lys Lys Leu Glu Asn Gly Val
675 680 685

Asp Arg Tyr Val Ser Lys Tyr Glu Ile Asp Gly Asn His Val Leu Leu
690 695 700

Tyr Leu Asp Lys Val Ser His Ser Glu Thr Glu Cys Val Gly Phe Lys
705 710 715 720

Ile His Gln Asp Phe Glu Val Gly Leu Leu Gln Pro Ala Ser Val Lys
725 730 735

Val Tyr Asp Tyr Tyr Glu Pro Asp Glu Gln Cys Thr Ala Phe Tyr
740 745 750

<210> 81

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Alpha-2-macroglobulin family N-terminal region

Consensus Sequence

<400> 81

Arg Leu Leu Trp Leu Leu Leu Leu Leu Leu Phe Phe Asp Ser Ser
1 5 10 15

Leu Gln Lys Pro Arg Tyr Met Val Ile Val Pro Ser Ile Leu Arg Thr
20 25 30

Glu Thr Pro Glu Lys Val Cys Val Gln Leu His Asp Leu Asn Glu Thr
35 40 45

Val Thr Val Thr Val Ser Leu His Ser Phe Pro Gly Lys Arg Asn Leu
50 55 60

Ser Ser Leu Phe Thr Val Leu Leu Ser Ser Lys Asp Leu Phe His Cys
65 70 75 80

Val Ser Phe Thr Val Pro Gln Pro Gly Leu Phe Lys Ser Ser Lys Gly
85 90 95

Glu Glu Ser Phe Val Val Val Gln Val Lys Gly Pro Thr His Thr Phe
100 105 110

Lys Glu Lys Val Thr Val Leu Val Ser Ser Arg Arg Gly Leu Val Phe
115 120 125

Ile Gln Thr Asp Lys Pro Ile Tyr Thr Pro Gly Gln Thr Val Arg Tyr
130 135 140

Arg Val Phe Ser Val Asp Glu Asn Leu Arg Pro Leu Asn Glu Leu Ile
145 150 155 160

Leu Val Tyr Ile Glu Asp Pro Glu Gly Asn Arg Val Asp Gln Trp Glu
 165 170 175
 Val Asn Lys Leu Glu Gly Gly Ile Phe Gln Leu Ser Phe Pro Ile Pro
 180 185 190
 Ser Glu Pro Ile Gln Gly Thr Trp Lys Ile Val Ala Arg Tyr Glu Ser
 195 200 205
 Gly Pro Glu Ser Asn Tyr Thr His Tyr Phe Glu Val Lys Glu Tyr Val
 210 215 220
 Leu Pro Ser Phe Glu Val Ser Ile Thr Pro Pro Lys Pro Phe Ile Tyr
 225 230 235 240
 Tyr Asp Asn Phe Lys Glu Phe Glu Val Thr Ile Cys Ala Arg Tyr Thr
 245 250 255
 Tyr Gly Lys Pro Val Pro Gly Val Ala Tyr Val Arg Phe Gly Val Lys
 260 265 270
 Asp Glu Asp Gly Lys Lys Glu Leu Leu Ala Gly Leu Glu Glu Arg Ala
 275 280 285
 Lys Leu Leu Asp Gly Asn Gly Glu Ile Cys Leu Ser Gln Glu Val Leu
 290 295 300
 Leu Lys Glu Leu Gln Leu Lys Asn Glu Asp Leu Glu Gly Lys Ser Leu
 305 310 315 320
 Tyr Val Ala Val Ala Val Ile Glu Ser Glu Gly Gly Asp Met Glu Glu
 325 330 335
 Ala Glu Leu Gly Gly Ile Lys Ile Val Arg Ser Pro Tyr Lys Leu Lys
 340 345 350
 Phe Val Lys Thr Pro Ser His Phe Lys Pro Gly Ile Pro Phe Phe Leu
 355 360 365
 Lys Val Leu Val Val Asp Pro Asp Gly Ser Pro Ala Pro Asn Val Pro
 370 375 380
 Val Lys Val Ser Ala Gln Asp Ala Ser Tyr Tyr Ser Asn Gly Thr Thr
 385 390 395 400
 Asp Glu Asp Gly Leu Ala Gln Phe Ser Ile Asn Thr Ser Gly Ile Ser
 405 410 415
 Ser Leu Ser Ile Thr Val Arg Thr Asn His Lys Glu Leu Pro Glu Glu
 420 425 430
 Val Gln Ala His Ala Glu Ala Gln Ala Thr Ala Tyr Ser Thr Val Ser
 435 440 445
 Leu Ser Lys Ser Tyr Ile His Leu Ser Ile Glu Arg Thr Leu Pro Cys
 450 455 460

Gly Pro Gly Val Gly Glu Gln Ala Asn Phe Ile Leu Arg Gly Lys Ser
 465 470 475 480
 Leu Gly Glu Leu Lys Ile Leu His Phe Tyr Tyr Leu Ile Met Ser Lys
 485 490 495
 Gly Lys Ile Val Lys Thr Gly Arg Glu Pro Arg Glu Pro Gly Gln Gly
 500 505 510
 Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe
 515 520 525
 Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp
 530 535 540
 Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu
 545 550 555 560
 Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys
 565 570 575
 Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val
 580 585 590
 Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser
 595 600 605
 Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly
 610 615 620

<210> 82
 <211> 186
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sodium Bile
 acid symporter family consensus sequence

<400> 82
 Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg
 1 5 10 15
 Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu
 20 25 30
 Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu
 35 40 45
 Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile
 50 55 60
 Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr
 65 70 75 80
 Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser

85										90					95															
Thr	Leu	Leu	Ala	Pro	Leu	Val	Thr	Pro	Leu	Leu	Ser	Phe	Leu	Leu	Ala															
			100						105					110																
Gly	Leu	Leu	Val	His	Val	Asp	Ala	Val	Ser	Pro	Trp	Ser	Leu	Ile	Lys															
		115					120						125																	
Ser	Val	Leu	Val	Tyr	Val	Ile	Ile	Pro	Leu	Ile	Ala	Gly	Met	Leu	Thr															
		130					135					140																		
Arg	Tyr	Phe	Leu	Pro	Glu	Trp	Phe	Glu	Gln	Arg	Val	Leu	Pro	Val	Leu															
					150					155					160															
Ser	Pro	Ile	Ser	Leu	Ile	Gly	Leu	Leu	Leu	Thr	Ile	Val	Val	Ile	Phe															
				165					170					175																
Ala	Leu	Asn	Gly	Glu	Val	Ile	Ala	Ser	Leu																					
			180					185																						

<210> 83
 <211> 191
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SPFH
 domain/Band 7 family Consensus Sequence

<400> 83
 Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val
 1 5 10 15
 Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg
 20 25 30
 Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe
 35 40 45
 Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val
 50 55 60
 Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp
 65 70 75 80
 Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu
 85 90 95
 Val Glu Asp Ala Glu Arg Ala Leu Pro Gln Leu Ala Gln Thr Thr Leu
 100 105 110
 Arg Asn Val Ile Gly Gln Phe Thr Leu Asp Glu Ile Leu Thr Glu Arg
 115 120 125
 Glu Arg Ile Asn Ser Gln Leu Arg Glu Ile Leu Asp Glu Ala Thr Asp
 130 135 140

Pro Trp Gly Ile Lys Val Glu Arg Val Glu Ile Lys Asp Ile Arg Leu
 145 150 155 160

Pro Glu Glu Val Gln Arg Ala Met Ala Ala Gln Met Glu Ala Glu Arg
 165 170 175

Glu Ala Arg Ala Lys Ile Leu Glu Ala Glu Gly Glu Gln Glu Ala
 180 185 190

<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin
 homologues Consensus Sequence

<400> 84

Ala Ala Phe Tyr Val Ile Gly Glu Gly Glu Arg Gly Val Val Glu Arg
 1 5 10 15

Leu Gly Arg Val Leu Lys Val Leu Gly Pro Gly Leu His Phe Val Ile
 20 25 30

Pro Phe Ile Asp Asp Val Lys Arg Val Asp Leu Arg Ala Gln Thr Asp
 35 40 45

Asp Val Pro Pro Gln Glu Val Ile Thr Lys Asp Asn Val Thr Val Ser
 50 55 60

Val Asp Ala Val Val Tyr Tyr Arg Val Leu Asp Pro Leu Lys Ala Val
 65 70 75 80

Tyr Gly Val Leu Asp Ala Asp Tyr Arg Ala Leu Arg Gln Leu Ala Gln
 85 90 95

Thr Thr Leu Arg Ser Val Ile Gly Lys Arg Thr Leu Asp Glu Leu Leu
 100 105 110

Thr Asp Glu Arg Glu Lys Ile Ser Glu Asn Ile Arg Glu Glu Leu Asn
 115 120 125

Glu Ala Ala Glu Pro Trp Gly Ile Glu Val Glu Asp Val Glu Ile Lys
 130 135 140

Asp Ile Arg Leu Pro Glu Glu Ile Lys Glu Ala Met Glu Ala Gln Gln
 145 150 155 160

<210> 85

<211> 79

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 85

Cys Tyr His Gly Asn Gly Glu Asn Tyr Arg Gly Thr Ala Ser Thr Thr
1 5 10 15

Glu Ser Gly Ala Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro His Arg
20 25 30

His Ser Lys Tyr Thr Pro Glu Arg Tyr Pro Ala Lys Gly Leu Gly Glu
35 40 45

Asn Tyr Cys Arg Asn Pro Asp Gly Asp Glu Arg Pro Trp Cys Tyr Thr
50 55 60

Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys
65 70 75

<210> 86

<211> 83

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 86

Arg Asp Cys Tyr Ala Gly Asn Gly Glu Ser Tyr Arg Gly Thr Ala Ser
1 5 10 15

Thr Thr Lys Ser Gly Lys Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro
20 25 30

His Leu His Arg Phe Thr Pro Glu Arg Phe Pro Glu Leu Gly Leu Glu
35 40 45

His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ser Glu Gly Pro Trp Cys
50 55 60

Tyr Thr Thr Asp Pro Asn Val Arg Trp Glu Tyr Cys Asp Ile Pro Gln
65 70 75 80

Cys Glu Ser

<210> 87

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

<400> 87

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
20 25 30

Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
35 40 45

Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
50 55 60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
65 70 75 80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
85 90 95

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
115 120 125

Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
145 150 155 160

Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
165 170 175

Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
180 185 190

Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
195 200 205

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
210 215 220

Ser Tyr Leu Asp Trp Ile
225 230

<210> 88

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin
Consensus Sequence

<400> 88

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
20 25 30

Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
35 40 45

Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
50 55 60

Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
65 70 75 80

Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
85 90 95

Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
100 105 110

Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
115 120 125

Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
130 135 140

Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
145 150 155 160

Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
165 170 175

Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
180 185 190

Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
195 200 205

Arg Val Ser Arg Tyr Leu Asp Trp Ile
210 215

<210> 89

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Divergent
subfamily of APPLE domains Consensus Sequence

<400> 89

Lys Ser Asp Asp Cys Phe Val Arg Leu Pro Asn Thr Lys Leu Pro Asp
1 5 10 15

Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln
20 25 30

Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn
35 40 45

Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala
50 55 60

Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile
65 70 75

<210> 90

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Lipocalin/cytosolic fatty-acid binding protein
family Consensus Sequence

<400> 90

Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro
1 5 10 15

Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile
20 25 30

Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys
35 40 45

Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys
50 55 60

Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val
65 70 75 80

Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly
85 90 95

Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro
100 105 110

Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu
115 120 125

Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg
130 135 140

Cys

145

<210> 91
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Connexin
 Consensus Sequence

<400> 91
 Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His
 1 5 10 15
 Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg
 20 25 30
 Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln
 35 40 45
 Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys
 50 55 60
 Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln
 65 70 75 80
 Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala
 85 90 95
 Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His
 100 105 110
 Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu
 115 120 125
 Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe
 130 135 140
 Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln
 145 150 155 160
 Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg
 165 170 175
 Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu
 180 185 190
 Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu
 195 200 205
 Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu
 210 215

<210> 92
 <211> 59

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Src homology 3
domains Consensus Sequence

<400> 92

Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro
1 5 10 15

Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys
20 25 30

Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly
35 40 45

Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp
50 55

<210> 93

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SH3 domain
Consensus Sequence

<400> 93

Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu
1 5 10 15

Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp
20 25 30

Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu
35 40 45

Ile Pro Ser Asn Tyr Val Glu Pro Val
50 55

<210> 94

<211> 91

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4
homology domain Consensus Sequence

<400> 94

Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser
1 5 10 15

Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met
20 25 30

Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys
35 40 45

Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly
50 55 60

Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu
65 70 75 80

Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu
85 90

<210> 95

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4
homology domain Consensus Sequence

<400> 95

Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu
1 5 10 15

Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe
20 25 30

Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln
35 40 45

His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu
50 55 60

Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr
65 70 75 80

Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu
85 90

<210> 96

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

<400> 96

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
 20 25 30
 Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
 35 40 45
 Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 50 55 60
 Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
 65 70 75 80
 Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
 85 90 95
 Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
 100 105 110
 Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125
 Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
 130 135 140
 Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
 145 150 155 160
 Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
 165 170 175
 Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 180 185 190
 Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
 195 200 205
 Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
 210 215 220
 Ser Tyr Leu Asp Trp Ile
 225 230

<210> 97

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin
 Consensus Sequence

<400> 97

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
 1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
 20 25 30
 Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
 35 40 45
 Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
 50 55 60
 Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
 55 70 75 80
 Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
 85 90 95
 Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
 100 105 110
 Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
 115 120 125
 Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
 130 135 140
 Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
 145 150 155 160
 Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
 165 170 175
 Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
 180 185 190
 Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
 195 200 205
 Arg Val Ser Arg Tyr Leu Asp Trp Ile
 210 215

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV5 Primer 1

<400> 98
 ctccactcc tgcgtcttct gact

24

<210> 99
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV5 Primer 2

 <400> 99
 aaggctgggc ctaaccagc ctcac 25

 <210> 100
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV7 Primer 1

 <400> 100
 catgaactgg gcatttctgc agg 23

 <210> 101
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV7 Primer 2

 <400> 101
 ttatctgctg atctcgcagg ttatgga 27

 <210> 102
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 1

 <400> 102
 ctgacaggcc ctggtgtgtg at 22

 <210> 103
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 2

 <400> 103
 tcacacatgt ttcattgtgg agttaga 27

 <210> 104
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 1

 <400> 104
 gagtgagagg tcggacagac tgtg 24

 <210> 105
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 2

 <400> 105
 actcatgcaa cttgcttctc tcactct 27

 <210> 106
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 1

 <400> 106
 cctatgagcc tgatgctgga tgac 24

 <210> 107
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 2

 <400> 107
 aggactcaga ggaggaggatc ctgag 25

 <210> 108
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward

 <400> 108

gcactacaag tggaagcctt ac 22

<210> 109
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 109
ctcaagtaga agccgactta tgcaaa 26

<210> 110
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 110
tcaaatcctt ctgcatata gt 22

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1313b
Forward

<400> 111
cagctgcacg attaatgaag at 22

<210> 112
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1313b Probe

<400> 112
aggtcttgga ctggccttca ccatt 25

<210> 113
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

<400> 113
 ccaaagttgt gtccagactc at 22

<210> 114
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Forward

<400> 114
 ccaaggaaga cctcttcac tt 22

<210> 115
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Probe

<400> 115
 tcttgcttac ggcataagcg ctctct 26

<210> 116
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

<400> 116
 ttcatttcta tgggacctca ga 22

<210> 117
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag708 Forward

<400> 117
 aaagatggga ctcgtcatga c 21

<210> 118

<211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Probe

 <400> 118
 cacgccatct tactgactgg tctgga 26

 <210> 119
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Reverse

 <400> 119
 gtgcaaattcc caaagtgtca 20

 <210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward

 <400> 120
 gcactacaag tggaagcctt ac 22

 <210> 121
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Probe

 <400> 121
 ctcaagtaga agccgactta tgcaaa 26

 <210> 122
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Reverse

 <400> 122
 tcaaattcctt ctgcgatata gt 22

<210> 123
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 123
ccaaggaaga cctcttcac tt 22

<210> 124
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 124
tcttgcttac ggcataagcg ctctct 26

<210> 125
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125
ttcatttcta tgggacctca ga 22

<210> 126
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 126
ccaaggaaga cctcttcac tt 22

<210> 127
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 127
tcttgcttac ggcataagcg ctctct 26

<210> 128
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 128
ttcatttcta tgggacctca ga 22

<210> 129
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Forward

<400> 129
aaagatggga ctcgcatga c 21

<210> 130
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Probe

<400> 130
cacgccatct tactgactgg tctgga 26

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Reverse

<400> 131
gtgcaaattcc caaagtgtca 20

<210> 132
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b
 Forward

<400> 132
 cagctgcacg attaatgaag at 22

<210> 133
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b Probe

<400> 133
 aggtcttgga ctggccttca ccatt 25

<210> 134
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

<400> 134
 ccaaagttgt gtccagactc at 22

<210> 135
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1537 Forward

<400> 135
 tttcaagaca ccctgtgata cc 22

<210> 136
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1537 Probe

<400> 136
 acttcgtgtc ctgaatgttc caggct 26

<210> 137
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1537 Reverse

 <400> 137
 cagaggaatg aaggcataga tg 22

 <210> 138
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2432 Forward

 <400> 138
 gtaggcaaag ggactcactg t 21

 <210> 139
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2432 Probe

 <400> 139
 cagaaatcaa taatctttga ctgccg 26

 <210> 140
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2432 Reverse

 <400> 140
 gcacattacg tggctgaga 19

 <210> 141
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1250 Forward

<400> 141
cgtggtgaac tctgccttat at 22

<210> 142
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1250 Probe

<400> 142
cacagagctg tcgtctttga ccgatt 26

<210> 143
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1250 Reverse

<400> 143
agtccctttg cctaccacaa t 21

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag3086 Forward

<400> 144
ggacccatt cgactactgt 20

<210> 145
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag3086 Probe

<400> 145
ctgatgacca gccgccatca atc 23

<210> 146
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Reverse

 <400> 146
 ttctcaaact gcacctgggc 20

 <210> 147
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Forward

 <400> 147
 tctggacgac aactattgcc 20

 <210> 148
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Probe

 <400> 148
 atggtgctac actacggatc cgcag 25

 <210> 149
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Reverse

 <400> 149
 gtcacagaat tctcgtctga 20

 <210> 150
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Forward

 <400> 150
 tatcatcact tgtgatggca aa 22

 <210> 151
 <211> 26

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Probe

 <400> 151
 aaaaccgaga gcactttgaa aacaca 26

 <210> 152
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Reverse

 <400> 152
 aaacttctct cccagggtag aa 22

 <210> 153
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Forward

 <400> 153
 tgaacagaac tatgcgaaac aa 22

 <210> 154
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Probe

 <400> 154
 tctgggtaag aagtactgcc ccaaacg 27

 <210> 155
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Reverse

 <400> 155
 ggctcttcat ctttggatga a 21

<210> 156
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1674 Forward

<400> 156
ctcactcacc acaagggagt aa 22

<210> 157
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1674 Probe

<400> 157
tgacatcaaa ctcaacagtt cccagga 27

<210> 158
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1674 Reverse

<400> 158
gtctaggaga gagctgagca aa 22

<210> 159
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PAN domain
Consensus Sequence

<400> 159
Cys Ser Ser Phe Val Arg Val Pro Gly Arg Ser Leu Ser Gly Asn Asp
1 5 10 15

Ile Ser Val Val Asn Val Pro Ser Leu Glu Glu Cys Ala Ala Leu Cys
20 25 30

Leu Glu Glu Pro Arg Val Cys Arg Ser Phe Thr Tyr Asn Asn Lys Ser
35 40 45

Lys Gln Cys Leu Leu Lys Ser Glu Ser Ser Gly Ser Leu Pro Arg Leu

50

55

60

Lys Arg Pro Ser Gln Lys Val Asp Tyr Tyr Glu Lys Ser Cys
 65 70 75

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin
 homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln
 1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His
 20 25 30

Val Arg